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<110> Bristol-Myers Squibb Company

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<151> 2000-12-04

<150> 60/263,678

<151> 2001-01-23

<150> 60/273,037

<151> 2001-03-02

<160> 1579

<170> PatentIn version 3.0

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Tyr Leu Pro Val	Thr Val Val Asn Thr Thr Met Ser Leu Thr Ala Leu				
cgc cag cag atg	cag acc cag aat ctc tca gcc tac atc atc cca ggc	60	65	70	483
Arg Gln Gln Met	Gln Thr Gln Asn Ile Leu Ser Ala Tyr Ile Pro Gly				
aca gat gct cac	atg aac gag tac atc ggc caa cat gac gag agg cgt	75	80	85	531
Thr Asp Ala His	Met Asn Glu Tyr Ile Gly Gln His Asp Glu Arg Arg				
gcg tgg att aca	ggc ttt aca ggg tct gca gga act gca gtg gtg act	90	95	100	579
Ala Trp Ile Thr	Gly Phe Thr Gly Ser Ala Gly Thr Ala Val Val Thr			105	
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Glu Arg Gln Met	Asp Cys Asn Trp Glu Leu His Lys Glu Val Gly Thr				
act cct att gtc	acc tgg ctc ctc acc gag att ccc gct gga ggg cgt	140	145	150	723
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gtg ggt ttt gac	ccc ttc ctc ttg tcc att gac acc tgg gag agt tat	155	160	165	771
Val Gly Phe Asp	Pro Phe Leu Leu Ser Ile Asp Thr Trp Glu Ser Tyr				
gat ctg gcc ctc	caa ggc tct aac aga cag ctg gtg tcc atc aca acc	170	175	180	819
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Asn Leu Val Asp	Leu Val Trp Gly Ser Glu Arg Pro Pro Val Pro Asn				
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Gln Pro Ile Tyr	Ala Phe Gln Glu Ala Phe Thr Gly Ser Thr Trp Gln				
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Pro Thr Ala Val	Leu Leu Ser Ala Leu Glu Glu Thr Ala Trp Leu Phe				
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 ggcattcgag gagccctttg aactttccaa agtcagacca cagctacaat gctgttaaat 3093
 cctcccacat ttcttgatg ccccttcacc ttgtgtggac agtgtctggt ttccccattt 3153
 tacagacagg aaaactgagc ttcagacagg ggggtgggctt tgccaaagga cacacaaatt 3213
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 atgcagagtc cctgagccca cctccagcc ctctctcat tctctgaacc cactgtggtg 3333
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35 40 45

Asn Thr Thr Met Ser Leu Thr Ala Leu Arg Gln Gln Met Gln Thr Gln
50 55 60

Asn Leu Ser Ala Tyr Ile Ile Pro Gly Thr Asp Ala His Met Asn Glu
65 70 75 80

Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr
 85 90 95

Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp
 100 105 110

Thr Asp Ser Arg Tyr Trp Thr Gln Ala Glu Arg Gln Met Asp Cys Asn
 115 120 125

Trp Glu Leu His Lys Glu Val Gly Thr Thr Pro Ile Val Thr Trp Leu
 130 135 140

Leu Thr Glu Ile Pro Ala Gly Gly Arg Val Gly Phe Asp Pro Phe Leu
 145 150 155 160

Leu Ser Ile Asp Thr Trp Glu Ser Tyr Asp Leu Ala Leu Gln Gly Ser
 165 170 175

Asn Arg Gln Leu Val Ser Ile Thr Thr Asn Leu Val Asp Leu Val Trp
 180 185 190

Gly Ser Glu Arg Pro Pro Val Pro Asn Gln Pro Ile Tyr Ala Leu Gln
 195 200 205

Glu Ala Phe Thr Gly Ser Thr Trp Gln Glu Lys Val Ser Gly Val Arg
 210 215 220

Ser Gln Met Gln Lys His Gln Lys Val Pro Thr Ala Val Leu Leu Ser
 225 230 235 240

Ala Leu Glu Glu Thr Ala Trp Leu Phe Asn Leu Arg Ala Ser Asp Ile
 245 250 255

Pro Tyr Asn Pro Phe Phe Tyr Ser Tyr Thr Leu Leu Thr Asp Ser Ser
 260 265 270

Ile Arg Leu Phe Ala Asn Lys Ser Arg Phe Ser Ser Glu Thr Leu Ser
 275 280 285

Tyr Leu Asn Ser Ser Cys Thr Gly Pro Met Cys Val Gln Ile Glu Asp
 290 295 300

Tyr Ser Gln Val Arg Asp Ser Ile Gln Ala Tyr Ser Leu Gly Asp Val
305 310 315 320

Arg Ile Trp Ile Gly Thr Ser Tyr Thr Met Tyr Gly Ile Tyr Glu Met
325 330 335

Ile Pro Arg Glu Lys Leu Val Thr Asp Thr Tyr Ser Pro Val Met Met
340 345 350

Thr Lys Ala Val Lys Asn Ser Lys Glu Gln Ala Leu Leu Lys Ala Ser
355 360 365

His Val Arg Asp Ala Val Ala Val Ile Arg Tyr Leu Val Trp Leu Glu
370 375 380

Lys Asn Val Pro Lys Gly Thr Val Asp Glu Phe Ser Gly Ala Glu Ile
385 390 395 400

Val Asp Lys Phe Arg Gly Glu Glu Gln Phe Ser Ser Gly Pro Ser Phe
405 410 415

Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser
420 425 430

Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu
435 440 445

Leu Asp Ser Gly Gly Gln Tyr Trp Asp Gly Thr Thr Asp Ile Thr Arg
450 455 460

Thr Val His Trp Gly Thr Pro Ser Ala Phe Gln Lys Glu Ala Tyr Thr
465 470 475 480

Arg Val Leu Ile Gly Asn Ile Asp Leu Ser Arg Leu Ile Phe Pro Ala
485 490 495

Ala Thr Ser Gly Arg Met Val Glu Ala Phe Ala Arg Arg Ala Leu Trp
500 505 510

Asp Ala Gly Leu Asn Tyr Gly His Gly Thr Gly His Gly Ile Gly Asn
515 520 525

Phe Leu Cys Val His Glu Trp Pro Val Gly Phe Gln Ser Asn Asn Ile

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Ala Met Ala Lys Gly Met Phe Thr Ser Ile Glu Pro Gly Tyr Tyr Lys
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Asp Gly Glu Phe Gly Ile Arg Leu Glu Asp Val Ala Leu Val Val Glu
565 570 575

Ala Lys Thr Lys Tyr Pro Gly Glu Leu Pro Asp Leu Val Val Ser Phe
580 585 590

Val Pro Tyr Asp Arg Asn Leu Ile Asp Val Ser Leu Leu Ser Pro Glu
595 600 605

His Leu Gln Tyr Leu Asn Arg Tyr Tyr Gln Thr Ile Arg Glu Lys Val
610 615 620

Gly Pro Glu Leu Gln Arg Arg Gln Leu Leu Glu Glu Phe Glu Trp Leu
625 630 635 640

Gln Gln His Thr Glu Pro Leu Ala Ala Arg Ala Pro Asp Thr Ala Ser
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Trp Ala Ser Val Leu Val Val Ser Thr Leu Ala Ile Leu Gly Trp Ser
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Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn
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Gln Ser Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro
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gaa gcc tgg gac ctg ctg cac aga gtg ctg ccg aca ttt atc atc tcc Glu Ala Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser 35 40 45	144
atc tgt ttc ttc ggc ctc cta ggg aac ctt ttt gtc ctg ttg gtc ttc Ile Cys Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe 50 55 60	192
ctc ctg ccc cgg cgg caa ctg aac gtg gca gaa atc tac ctg gcc aac Leu Leu Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn 65 70 75	240
ctg gca gcc tct gat ctg gtg ttt gtc ttg ggc ttg ccc ttc tgg gca Leu Ala Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala 80 85 90	288
gag aat atc tgg aac cag ttt aac tgg cct ttc gga gcc ctc ctc tgc Glu Asn Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys 95 100 105 110	336
cgt gtc atc aac ggg gtc atc aag gcc aat ttg ttc atc agc atc ttc Arg Val Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe 115 120 125	384
ctg gtg gtg gcc atc agc cag gac cgc tac cgc gtg ctg gtg cac cct Leu Val Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro 130 135 140	432
atg gcc agc gga agg cag cag cgg cgg agg cag gcc cgg gtc acc tgc Met Ala Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys 145 150 155	480
gtg ctc atc tgg gtt gtg ggg ggc ctc ttg agc atc ccc aca ttc ctg Val Leu Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu 160 165 170	528
ctg cga tcc atc caa gcc gtc cca gat ctg aac atc acc gcc tgc atc Leu Arg Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile 175 180 185 190	576
ctg ctc ctc ccc cat gag gcc tgg cac ttt gca agg att gtg gag tta Leu Leu Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu 195 200 205	624
aat att ctg ggt ttc ctc cta cca ctg gct gcg atc gtc ttc ttc aac Asn Ile Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn 210 215 220	672
tac cac atc ctg gcc tcc ctg cga acg cgg gag gag gtc agc agg aca Tyr His Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr 225 230 235	720
aga gtg cgg ggg ccg aag gat agc aag acc aca gcg ctg atc ctc acg Arg Val Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr 240 245 250	768
ctc gtg gtt gcc ttc ctg gtc tgc tgg gcc cct tac cac ttc ttt gcc	816

Leu Val Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala	
255 260 265 270	
ttc ctg gaa ttc tta ttc cag gtg caa gca gtc cga ggc tgc ttt tgg	864
Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp	
275 280 285	
gag gac ttc att gac ctg ggc ctg caa ttg gcc aac ttc ttt gcc ttc	912
Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe	
290 295 300	
act aac agc tcc ctg aat cca gta att tat gtc ttt gtg ggc cgg ctc	960
Thr Asn Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu	
305 310 315	
ttc agg acc aag gtc tgg gaa ctt tat aaa caa tgc acc cct aaa agt	1008
Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser	
320 325 330	
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Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys	
35 40 45	
Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu	
50 55 60	
Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala	
65 70 75 80	
Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn	
85 90 95	

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
225 230 235 240

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
325 330 335

Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
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Asn

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Gln Ser Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro
15 20 25 30
gaa gcc tgg gac ctg ctg cac aga gtg ctg ccg aca ttt atc atc tcc 144
Glu Ala Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser
35 40 45
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Ile Cys Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe
50 55 60
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Leu Leu Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn
65 70 75
ctg gca gcc tct gat ctg gtg ttt gtc ttg ggc ttg ccc ttc tgg gca 288
Leu Ala Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala
80 85 90
gag aat atc tgg aac cag ttt aac tgg cct ttc gga gcc ctg ctg tgc 336
Glu Asn Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys
95 100 105 110
cgt gtc atc aac ggg gtc atc aag gcc aat ttg ttc atc agc atc ttc 384
Arg Val Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe
115 120 125
ctg gtg gtg gcc atc agc cag gac cgc tac cgc gtg ctg gtg cac cct 432
Leu Val Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro

130	135	140	
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Met Ala Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys			
145	150	155	
gtg ctc atc tgg gtt gtg ggg ggc ctc ttg agc atc ccc aca ttc ctg			528
Val Leu Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu			
160	165	170	
ctg cga tcc atc caa gcc gtc cca gat ctg aac atc acc gcc tgc atc			576
Leu Arg Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile			
175	180	185	190
ctg ctc ctc ccc cat gag gcc tgg cac ttt gca agg att gtg gag tta			624
Leu Leu Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu			
195	200	205	
aat att ctg ggt ttc ctc cta cca ctg gct gcg atc gtc ttc ttc aac			672
Asn Ile Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn			
210	215	220	
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Tyr His Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr			
225	230	235	
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Arg Val Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr			
240	245	250	
ctc gtg gtt gcc ttc ctg gtc tgc tgg gcc cct tac cac ttc ttt gcc			816
Leu Val Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala			
255	260	265	270
ttc ctg gaa ttc tta ttc cag gtg caa gca gtc cga ggc tgc ttt tgg			864
Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp			
275	280	285	
gag gac ttc att gac ctg ggc ctg caa ttg gcc aac ttc ttt gcc ttc			912
Glu Asp Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe			
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act aac agc tcc ctg aat cca gta att tat gtc ttt gtg ggc cag ctc			960
Thr Asn Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Gln Leu			
305	310	315	
ttc agg acc aag gtc tgg gaa ctt tat aaa caa tgc acc cct aaa agt			1008
Phe Arg Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser			
320	325	330	
ctt gct cca ata tct tca tcc cat agg aaa gaa atc ttc caa ctt ttc			1056
Leu Ala Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe			
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Trp Arg Asn			

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Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
 50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
 65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
 100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
 130 135 140

Ser Gly Arg Gln Gln Arg Arg Gln Ala Arg Val Thr Cys Val Leu
 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
 165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
 180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
225 230 235 240

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Gln Leu Phe Arg
305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
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Phe Leu Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp
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320 325 330

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35 40 45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala

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Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
225 230 235 240

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
305 310 315 320

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325 330 335

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Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr
20 25 30
ttg caa ggg ccc act ctt aac ggg acc ttt gcc cag agc aaa tgc ccc 144
Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro
35 40 45
caa gtg gag tgg ctg gcc tgg ctc aac acc atc cag ccc ccc ttc ctc 192
Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu
50 55 60
tgg gtg ctg ttc gtg ctg gcc acc cta gag aac atc ttt gtc ctc agc 240
Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser
65 70 75 80
gtc ttc tgc ctg cac aag agc agc tgc acg gtg gca gag atc tac ctg 288
Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu
85 90 95
ggg aac ctg gcc gca gca gac ctg atc ctg gcc tgc ggg ctg ccc ttc 336
Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe
100 105 110
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Trp	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Phe	Asp	Trp	Leu	Phe	Gly	Glu	Thr		
	115						120					125					
ctc	tgc	cgc	gtg	gtg	aat	gcc	att	atc	tcc	atg	aac	ctg	tac	agc	agc	432	
Leu	Cys	Arg	Val	Val	Asn	Ala	Ile	Ile	Ser	Met	Asn	Leu	Tyr	Ser	Ser		
	130					135					140						
atc	tgt	ttc	ctg	atg	ctg	gtg	agc	atc	gac	cgc	tac	ctg	gcc	ctg	gtg	480	
Ile	Cys	Phe	Leu	Met	Leu	Val	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Leu	Val		
	145				150				155					160			
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Lys	Thr	Met	Ser	Met	Gly	Arg	Met	Arg	Gly	Val	Arg	Trp	Ala	Lys	Leu		
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Tyr	Ser	Leu	Val	Ile	Trp	Gly	Cys	Thr	Leu	Leu	Leu	Ser	Ser	Pro	Met		
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ctg	gtg	ttc	cgg	acc	atg	aag	gag	tac	agc	gat	gag	ggc	cac	aac	gtc	624	
Leu	Val	Phe	Arg	Thr	Met	Lys	Glu	Tyr	Ser	Asp	Glu	Gly	His	Asn	Val		
			195				200					205					
acc	gct	tgt	gtc	atc	agc	tac	cca	tcc	ctc	atc	tgg	gaa	gtg	ttc	acc	672	
Thr	Ala	Cys	Val	Ile	Ser	Tyr	Pro	Ser	Leu	Ile	Trp	Glu	Val	Phe	Thr		
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aac	atg	ctc	ctg	aat	gtc	gtg	ggc	ttc	ctg	ctg	ccc	ctg	agt	gtc	atc	720	
Asn	Met	Leu	Leu	Asn	Val	Val	Gly	Phe	Leu	Leu	Pro	Leu	Ser	Val	Ile		
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acc	ttc	tgc	acg	atg	cag	atc	atg	cag	gtg	ctg	cgg	aac	aac	gag	atg	768	
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Gln	Lys	Phe	Lys	Glu	Ile	Gln	Thr	Glu	Arg	Arg	Ala	Thr	Val	Leu	Val		
			260					265					270				
ctg	gtt	gtg	ctg	ctg	cta	ttc	atc	atc	tgc	tgg	ctg	ccc	ttc	cag	atc	864	
Leu	Val	Val	Leu	Leu	Phe	Ile	Ile	Ile	Cys	Trp	Leu	Pro	Phe	Gln	Ile		
			275			280						285					
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Ser	Thr	Phe	Leu	Asp	Thr	Leu	His	Arg	Leu	Gly	Ile	Leu	Ser	Ser	Cys		
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Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu
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Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
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Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val
145 150 155 160

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu
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Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr
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Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile
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Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val
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Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys
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Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met
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Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly
325 330 335

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Met Asp Asn Val Leu Pro Val Asp
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gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile 45 50 55	378
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Ser	Asp	Arg	Tyr	His	Glu	Gln	Val	Ser	Ala	Lys	Arg	Lys	Val	Val	Lys		
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atg	atg	att	gtc	gtg	gtg	tgc	acc	ttc	gcc	atc	tgc	tgg	ctg	ccc	ttc	1002	
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cac	atc	ttc	ttc	ctc	ctg	ccc	tac	atc	aac	cca	gat	ctc	tac	ctg	aag	1050	
His	Ile	Phe	Phe	Leu	Leu	Pro	Tyr	Ile	Asn	Pro	Asp	Leu	Tyr	Leu	Lys		
	265				270				275						280		
aag	ttt	atc	cag	cag	gtc	tac	ctg	gcc	atc	atg	tgg	ctg	gcc	atg	agc	1098	
Lys	Phe	Ile	Gln	Gln	Val	Tyr	Leu	Ala	Ile	Met	Trp	Leu	Ala	Met	Ser		
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Ser	Thr	Met	Tyr	Asn	Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Asp	Arg	Phe		
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Arg	Leu	Gly	Phe	Lys	His	Ala	Phe	Arg	Cys	Cys	Pro	Phe	Ile	Ser	Ala		
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ggc	gac	tat	gag	ggg	ctg	gaa	atg	aaa	tcc	acc	cgg	tat	ctc	cag	acc	1242	
Gly	Asp	Tyr	Glu	Gly	Leu	Glu	Met	Lys	Ser	Thr	Arg	Tyr	Leu	Gln	Thr		
			330			335						340					
cag	ggc	agt	gtg	tac	aaa	gtc	agc	cgc	ctg	gag	acc	acc	atc	tcc	aca	1290	
Gln	Gly	Ser	Val	Tyr	Lys	Val	Ser	Arg	Leu	Glu	Thr	Thr	Ile	Ser	Thr		
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Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
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Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
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Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
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Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
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Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
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Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
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Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
 145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
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Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
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Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
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Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu
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Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile
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Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe
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Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met
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Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser
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 cagatagtag gctttacgcc tagcttcgaa atg gat aac gtc ctc ccg gtg gac 234
 Met Asp Asn Val Leu Pro Val Asp
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 Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr
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 Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile
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 aac ctg gcc ttc gcg gag gcc tcc atg gct gca ttc aat aca gtg gtg 474
 Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val
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 aac ttc acc tat gct gtc cac aac gaa tgg tac tac ggc ctg ttc tac 522
 Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr
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 Cys Lys Phe His Asn Phe Phe Pro Ile Ala Ala Val Phe Ala Ser Ile
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Pro Glu His Pro Asn Lys Ile Tyr Glu Lys Val	185 190 195 200	
act gtg ctg atc tac ttc ctc ccc ctg ctg gtg att ggc tat gca tac	858	
Thr Val Leu Ile Tyr Phe Leu Pro Leu Leu Val Ile Gly Tyr Ala Tyr	205 210 215	
acc gta gtg gga atc aca cta tgg gcc agt gag atc ccc ggg gac tcc	906	
Thr Val Val Gly Ile Thr Leu Trp Ala Ser Glu Ile Pro Gly Asp Ser	220 225 230	
tct gac cgc tac cac gag caa gtc tct gcc aag cgc aag gtg gtc aaa	954	
Ser Asp Arg Tyr His Glu Gln Val Ser Ala Lys Arg Lys Val Val Lys	235 240 245	
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Met Met Ile Val Val Val Cys Thr Phe Ala Ile Cys Trp Leu Pro Phe	250 255 260	
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His Ile Phe Phe Leu Leu Pro Tyr Ile Asn Pro Asp Leu Tyr Leu Lys	265 270 275 280	
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Lys Phe Ile Gln Gln Val Tyr Leu Ala Ile Met Trp Leu Ala Met Ser	285 290 295	
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Ser Thr Met Tyr Asn Pro Ile Ile Tyr Cys Cys Leu Asn Asp Arg Phe	300 305 310	
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Arg Leu Gly Phe Lys His Ala Phe Arg Cys Cys Pro Phe Ile Ser Ala	315 320 325	
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Gln Gly Ser Val Tyr Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr	345 350 355 360	
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Val Val Gly Ala His Glu Glu Glu Pro Glu Asp Gly Pro Lys Ala Thr	365 370 375	
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Pro Ser Ser Leu Asp Leu Thr Ser Asn Cys Ser Ser Arg Ser Asp Ser	380 385 390	
aag acc atg aca gag agc ttc agc ttc tcc tcc aat gtg ctc tcc	1431	
Lys Thr Met Thr Glu Ser Phe Ser Phe Ser Ser Asn Val Leu Ser		

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Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val
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Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
 50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
 65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
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Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
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Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
 115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
 130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
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Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
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Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
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Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
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Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
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Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
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Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
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Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu
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Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile
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Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe
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Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met
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Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser
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Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu
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Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser
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Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser
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Phe Ser Ser Asn Val Leu Ser
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agaaggaccc tgagccccag gcgccagcca caggactctg ctgcagaggg gggttgtgta 180
cagatagtag gctttacgcc tagcttcgaa atg gat aac gtc ctc ccg gtg gac 234
Met Asp Asn Val Leu Pro Val Asp
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Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln
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Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr
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Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile
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Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val
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Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val
75 80 85
aac ttc acc tat gct gtc cac aac gaa tgg tac tac ggc ctg ttc tac 522
Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr
90 95 100
tgc aag ttc cac aac ttc ttt ccc atc gcc gct gtc ttc gcc agt atc 570

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Cys	Lys	Phe	His	Asn	Phe	Phe	Pro	Ile	Ala	Ala	Val	Phe	Ala	Ser	Ile	
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Tyr	Ser	Met	Thr	Ala	Val	Ala	Phe	Asp	Arg	Tyr	Met	Ala	Ile	Ile	His	
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Pro	Leu	Gln	Pro	Arg	Leu	Ser	Ala	Thr	Ala	Thr	Lys	Val	Val	Ile	Cys	
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Val	Ile	Trp	Val	Leu	Ala	Leu	Leu	Leu	Ala	Phe	Pro	Gln	Gly	Tyr	Tyr	
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Ser	Thr	Thr	Glu	Thr	Met	Pro	Ser	Arg	Val	Val	Cys	Met	Ile	Glu	Trp	
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Thr	Val	Leu	Ile	Tyr	Phe	Leu	Pro	Leu	Leu	Val	Ile	Gly	Tyr	Ala	Tyr	
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acc	gta	gtg	gga	atc	aca	cta	tgg	gcc	agt	gag	atc	ccc	ggg	gac	tcc	906
Thr	Val	Val	Gly	Ile	Thr	Leu	Trp	Ala	Ser	Glu	Ile	Pro	Gly	Asp	Ser	
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Ser	Asp	Arg	Tyr	His	Glu	Gln	Val	Ser	Ala	Lys	Arg	Lys	Val	Val	Lys	
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atg	atg	att	gtc	gtg	gtg	tgc	acc	ttc	gcc	atc	tgc	tgg	ctg	ccc	ttc	1002
Met	Met	Ile	Val	Val	Val	Cys	Thr	Phe	Ala	Ile	Cys	Trp	Leu	Pro	Phe	
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cac	atc	ttc	ttc	ctc	ctg	ccc	tac	atc	aac	cca	gat	ctc	tac	ctg	aag	1050
His	Ile	Phe	Phe	Leu	Leu	Pro	Tyr	Ile	Asn	Pro	Asp	Leu	Tyr	Leu	Lys	
	265				270				275						280	
aag	ttt	atc	cag	gac	gtc	tac	ctg	gcc	atc	atg	tgg	ctg	gcc	atg	agc	1098
Lys	Phe	Ile	Gln	Gln	Val	Tyr	Leu	Ala	Ile	Met	Trp	Leu	Ala	Met	Ser	
				285					290					295		
tcc	acc	atg	tac	aac	ccc	atc	atc	tac	tgc	tgc	ctc	aat	gac	agg	ttc	1146
Ser	Thr	Met	Tyr	Asn	Pro	Ile	Ile	Tyr	Cys	Cys	Leu	Asn	Asp	Arg	Phe	
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cgt	ctg	ggc	ttc	aag	cat	gcc	ttc	cgg	tgc	tgc	ccc	ttc	atc	agc	gcc	1194
Arg	Leu	Gly	Phe	Lys	His	Ala	Phe	Arg	Cys	Cys	Pro	Phe	Ile	Ser	Ala	
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ggc	gac	tat	gag	ggg	ctg	gaa	atg	aaa	tcc	acc	cgg	tat	ctc	cag	acc	1242
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Gln Gly Ser Val Tyr Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr			
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Val Val Gly Ala His Glu Glu Glu Pro Glu Asp Gly Pro Lys Ala Thr			
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Pro Ser Ser Leu Asp Leu Thr Ser Asn Cys Ser Ser Arg Ser Asp Ser			
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Lys Thr Met Thr Glu Ser Phe Ser Phe Ser Ser Asn Val Leu Ser			
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	20	25	30
Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val			
	35	40	45
Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg			
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Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser			
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			80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
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Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
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Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
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Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
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Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu
275 280 285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile
290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe
305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met
325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser
340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu
355 360 365

Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser
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agaaggacc ccagccccag cgcgccagcca caggactctg ctgcagaggg ggggttggtga 180
cagatagtag gctttacgcc tagcttogaa atg gat aac gtc ctc ccg gtg gac 234
Met Asp Asn Val Leu Pro Val Asp
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Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln
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Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr
25 30 35 40
gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc 378

1000
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Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile	
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Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val	
60 65 70	
aac ctg gcc ttc gcg gag gcc tcc atg gct gca ttc aat aca gtg gtg	474
Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val	
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Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr	
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Cys Lys Phe His Asn Phe Phe Pro Ile Ala Ala Val Phe Ala Ser Ile	
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Tyr Ser Met Thr Ala Val Ala Phe Asp Arg Tyr Met Ala Ile Ile His	
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Val Ile Trp Val Leu Ala Leu Leu Leu Ala Phe Pro Gln Gly Tyr Tyr	
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Ser Thr Thr Glu Thr Met Pro Ser Arg Val Val Cys Met Ile Glu Trp	
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Pro Glu His Pro Asn Lys Ile Tyr Glu Lys Val Tyr His Ile Cys Val	
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Thr Val Leu Ile Tyr Phe Leu Pro Leu Leu Val Ile Gly Tyr Ala Tyr	
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Thr Val Val Gly Ile Thr Leu Trp Ala Ser Glu Ile Pro Gly Asp Ser	
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Ser Asp Arg Tyr His Glu Gln Val Ser Ala Lys Arg Lys Val Val Lys	
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Lys Phe Ile Gln Gln Val Tyr Leu Ala Ile Met Trp Leu Ala Met Ser	285	290	295	
tcc acc atg tac aac ccc atc atc tac tgc tgc ctc aat gac agg ttc				1146
Ser Thr Met Tyr Asn Pro Ile Ile Tyr Cys Cys Leu Asn Asp Arg Phe	300	305	310	
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Arg Leu Gly Phe Lys His Ala Phe Arg Cys Cys Pro Phe Ile Ser Ala	315	320	325	
ggc gac tat gag ggg ctg gaa atg aaa tcc acc cgg tat ctc cag acc				1242
Gly Asp Tyr Glu Gly Leu Glu Met Lys Ser Thr Arg Tyr Leu Gln Thr	330	335	340	
cag ggc agt gtg tac aaa gtc agc cgc ctg gag acc acc atc tcc aca				1290
Gln Gly Ser Val Tyr Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr	345	350	355	360
gtg gtg ggg gcc cac gag gag gag cca gag gac ggc ccc aag gcc aca				1338
Val Val Gly Ala His Glu Glu Glu Pro Glu Asp Gly Pro Lys Ala Thr	365	370	375	
ccc tca tcc ctg gac ctg acc tcc aac tgc tct tca cga agt gac tcc				1386
Pro Ser Ser Leu Asp Leu Thr Ser Asn Cys Ser Ser Arg Ser Asp Ser	380	385	390	
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Lys Thr Met Thr Glu Ser Phe Ser Phe Ser Ser Asn Val Leu Ser	395	400	405	
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Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val
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Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
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Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
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Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
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Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Phe Pro
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Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
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Thr Ala Thr Lys Val Val Ile Cys Val Ile Trp Val Leu Ala Leu Leu
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Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
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Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
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Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
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Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
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Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
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Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
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Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
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Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu
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Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile
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Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe
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Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met
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Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser
340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu
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Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu Asp Leu Thr Ser
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cgg acc ctg tac agc agc agc ccc aga gtc cta agc aac aac agt gac	828						
Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp							
		245		250		255	
gcc aac ttg gag ctc atc aac acc tgg gtg gcc aag aac acc aac aac	876						
Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn							
		260		265		270	
aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt gtc	924						
Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val							
		275		280		285	
ctc ctc aat gct atc tac ctg agt gcc aag tgg aag aca aca ttt gat	972						
Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp							
		290		295		300	
ccc aag aaa acc aga atg gaa ccc ttt cac ttc aaa aac tca gtt ata	1020						
Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile							
		305		310		315	
aaa gtg ccc atg atg aat agc aag aag tac cct gtg gcc cat ttc att	1068						
Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile							
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gac caa act ttg aaa gcc aag gtg ggg cag ctg cag ctc tcc cac aat	1116						
Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn							
		340		345		350	
ctg agt ttg gtg atc ctg gta ccc cag aac ctg aaa cat cgt ctt gaa	1164						
Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu							
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Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu							
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aaa ctg gag atg tcc aag ttc cag ccc act ctc cta aca cta ccc cgc	1260						
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg							
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Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu							
		405		410		415	
gaa ttc ttc gat ttt tct tat gac ctt aac ctg tgt ggg ctg aca gag	1356						
Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu							
		420		425		430	
gac cca gat ctt cag gtt tct gcg atg cag cac cag aca gtg ctg gaa	1404						
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu							
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ctg aca gag act ggg gtg gag gcg gct gca gcc tcc gcc atc tct gtg	1452						
Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ser Ala Ile Ser Val							
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Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val
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ctc tgg gac cag cag cac aag ttc cct gtc ttc atg ggg cga gta tat 1548
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Asp Pro Arg Ala
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Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser
50 55 60

Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala
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Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr
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Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp
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Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr
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Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp
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Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met
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Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn
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Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
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Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn

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345

350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu
355 360 365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu
370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg
385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu
405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu
420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu
435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val
450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val
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<210> 23

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Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Ala

108

1	5	10	15	
ggg gat aga gcc tcc tca aat cca aat gct acc agc tcc agc tcc cag				156
Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln	20	25	30	
gat cca gag agt ttg caa gac aga ggc gaa ggg aag gtc gca aca aca				204
Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr	35	40	45	
gtt atc tcc aag atg cta ttc gtt gaa ccc atc ctg gag gtt tcc agc				252
Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser	50	55	60	
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Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala	65	70	75	80
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Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr	85	90	95	
caa ccc acc atc caa ccc acc caa cca act acc cag ctc cca aca gat				396
Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp	100	105	110	
tct cct acc cag ccc act act ggg tcc ttc tgc cca gga cct gtt act				444
Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr	115	120	125	
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Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp	130	135	140	
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Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met	145	150	155	160
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Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser	165	170	175	
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Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn	180	185	190	
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Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln	195	200	205	
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Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser
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Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr
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Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr

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120

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145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
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Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn
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Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
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Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
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Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
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Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
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Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
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Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
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Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
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Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
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Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn
340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu
355 360 365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu
370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg
385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu
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Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu
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Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val
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Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr	
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Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala	
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Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr	
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Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp	
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180 185 190	
ctg gag agc atc ctc tct tac ccc aag gac ttc acc tgt gtc cac cag	684
Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln	
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gcc ctg aag ggc ttc acg acc aaa ggt gtc acc tca gtc tct cag atc	732
Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile	
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Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser	
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aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt gtc Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val 275 280 285	924
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Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
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260 265 270

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290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
305 310 315 320

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325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Leu Ser His Asn
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Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu			370	375	380
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Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg			385	390	395
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Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu			405	410	415
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Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu			435	440	445
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Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ser Ala Ile Ser Val			450	455	460
gcc cgc acc ctg ctg gtc ttt gaa gtg cag cag ccc ttc ctc ttc gtg		1500			
Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val					

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Asp Pro Arg Ala	500			
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Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala				
65 70 75 80				
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100 105 110				
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Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn
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Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
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Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
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Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn
340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu
355 360 365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu
370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg
385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu
405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu
420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu
435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val
450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val
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Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser	
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Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala	
65 70 75	
aat acc act gat gaa ccc acc aca caa ccc acc aca gag ccc acc acc	348
Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr	
85 90 95	
caa ccc acc atc caa ccc acc caa cca act acc cag ctc cca aca gat	396
Gln Pro Thr Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp	
100 105 110	
tct cct acc cag ccc act act ggg tcc ttc tgc cca gga cct gtt act	444
Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr	
115 120 125	
ctc tgc tct gac ttg gag agt cat tca aca gag gcc gtg ttg ggg gat	492
Leu Cys Ser Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp	
130 135 140	
gct ttg gta gat ttc tcc ctg aag ctc tac cac gcc ttc tca gca atg	540
Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met	
145 150 155	
aag aag gtg gag acc aac atg gcc ttt tcc cca ttc agc atc gcc agc	588
Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser	
165 170 175	
ctc ctt acc cag gtc ctg ctc ggg gct ggg cag aac acc aaa aca aac	636
Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn	
180 185 190	
ctg gag agc atc ctc tct tac ccc aag gac ttc acc tgt gtc cac cag	684
Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln	
195 200 205	
gcc ctg aag ggc ttc acg acc aaa ggt gtc acc tca gtc tct cag atc	732
Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile	
210 215 220	
ttc cac agc cca gac ctg gcc ata agg gac acc ttt gtg aat gcc tct	780
Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser	
225 230 235	
cgg acc ctg tac agc agc agc ccc aga gtc cta agc aac aac agt gac	828
Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp	

245	250	255	
gcc aac ttg gag ctc atc aac acc tgg gtg gcc aag aac acc aac aac			876
Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn			
260	265	270	
aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt gtc			924
Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val			
275	280	285	
ctc ctc aat get atc tac ctg agt gcc aag tgg aag aca aca ttt gat			972
Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp			
290	295	300	
ccc aag aaa acc aga atg gaa ccc ttt cac ttc aaa aac tca gtt ata			1020
Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile			
305	310	315	320
aaa gtg ccc atg atg aat agc aag aag tac cct gtg gcc cat ttc att			1068
Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile			
325	330	335	
gac caa act ttg aaa gcc aag gtg ggg cag ctg cag ctc tcc cac aat			1116
Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn			
340	345	350	
ctg agt ttg gtg atc ctg gta ccc cag aac ctg aaa cat cgt ctt gaa			1164
Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu			
355	360	365	
gac atg gaa cag gct ctc agc cct tct gtt ttc aag gcc atc atg gag			1212
Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu			
370	375	380	
aaa ctg gag atg tcc aag ttc cag ccc act ctc cta aca cta ccc cgc			1260
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg			
385	390	395	400
atc aaa gtg acg acc agc cag gat atg ctc tca atc atg gag aaa ttg			1308
Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu			
405	410	415	
gaa ttc ttc gat ttt tct tat gac ctt aac ctg tgt ggg ctg aca gag			1356
Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu			
420	425	430	
gac cca gat ctt cag gtt tct gcg atg cag cac cag aca gtg ctg gaa			1404
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu			
435	440	445	
ctg aca gag act ggg gtg gag gcg gct gca gcc tcc gcc atc tct gtg			1452
Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ser Ala Ile Ser Val			
450	455	460	
gcc cgc acc ctg ctg gtc ttt gaa gtg cag cag ccc ttc ctc ttc atg			1500
Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Met			
465	470	475	480

ctc tgg gac cag cag cac aag ttc cct gtc ttc atg ggg cga gta tat 1548
 Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr
 485 490 495

gac ccc agg gcc tgagacctgc aggatcagggt tagggcgagc gctacctctc 1600
 Asp Pro Arg Ala
 500

cagcctcagc tctcagttgc agccctgctg ctgcctgcct ggacttgccc ctgccacctc 1660

ctgcctcagg tgtccgctat ccacaaaag ggctcctgag ggtctgggca agggacctgc 1720

ttctattagc ccttctccat ggcctcgcca tgctctccaa accacttttt gcagctttct 1780

ctagttcaag ttcaccagac tctataaata aaacctgaca gaccat 1826

<210> 30
 <211> 500
 <212> PRT
 <213> homo sapiens

<400> 30

Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Ala
 1 5 10 15

Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln
 20 25 30

Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr
 35 40 45

Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser
 50 55 60

Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala
 65 70 75 80

Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Asp
 85 90 95

Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp
 100 105 110

Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr
 115 120 125

Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp
130 135 140

Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met
145 150 155 160

Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
165 170 175

Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn
180 185 190

Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
195 200 205

Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
210 215 220

Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
225 230 235 240

Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
245 250 255

Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
260 265 270

Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
275 280 285

Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
290 295 300

Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
305 310 315 320

Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
325 330 335

Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Leu Ser His Asn
340 345 350

Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu

355

360

365

Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu
370 375 380

Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg
385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu
405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu
420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu
435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ser Ala Ile Ser Val
450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Met
465 470 475 480

Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr
485 490 495

Asp Pro Arg Ala
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<210> 31

<211> 871

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (37)..(822)

<400> 31

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Met Trp Phe Leu Val Leu
1 5

tgc ctc gcc ctg tcc ctg ggg ggg act ggt gct gcg ccc ccg att cag 102
Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly Ala Ala Pro Pro Ile Gln
10 15 20

tcc cgg att gtg gga ggc tgg gag tgt gag cag cat tcc cag ccc tgg	150
Ser Arg ile Val Gly Gly Trp Glu Cys Glu Gln His Ser Glu Gln Pro Trp	
25 30 35	
cag gcg gct ctg tac cat ttc agc act ttc cag tgt ggg ggc atc ctg	198
Gln Ala Ala Leu Tyr His Phe Ser Thr Phe Gln Cys Gly Gly Ile Leu	
40 45 50	
gtg cac cgc cag tgg gtg ctc aca gct gct cat tgc atc agc gac aat	246
Val His Arg Gln Trp Val Leu Thr Ala Ala His Cys Ile Ser Asp Asn	
55 60 65 70	
tac cag ctc tgg ctg ggt cgc cac aac ttg ttt gac gac gaa aac aca	294
Tyr Gln Leu Trp Leu Gly Arg His Asn Leu Phe Asp Asp Gly Phe Asn Thr	
75 80 85	
gcc cag ttt gtt cat gtc agt gag agc ttc cca cac cct ggc ttc aac	342
Ala Gln Phe Val His Val Ser Glu Ser Phe Pro His Pro Gly Phe Asn	
90 95 100	
atg agc ctc ctg gag aac cac acc cgc caa gca gac gag gac tac agc	390
Met Ser Leu Leu Glu Asn His Thr Arg Gln Ala Asp Glu Asp Tyr Ser	
105 110 115	
cac gac ctc atg ctg ctc cgc ctg aca gag cct gct gat acc atc aca	438
His Asp Leu Met Leu Leu Arg Leu Thr Glu Pro Ala Asp Thr Ile Thr	
120 125 130	
gat gct gtg aag gtc gtg gag ttg ccc acc gag gaa ccc gaa gtg ggg	486
Asp Ala Val Lys Val Val Glu Leu Pro Thr Glu Glu Pro Glu Val Gly	
135 140 145 150	
agc acc tgt ttg gct tcc ggc tgg ggc agc atc gaa cca gag aat ttc	534
Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Asn Phe	
155 160 165	
tca ttt cca gat gat ctc cag tgt gtg gac ctc aaa atc ctg cct aat	582
Ser Phe Pro Asp Asp Leu Gln Cys Val Asp Leu Lys Ile Leu Pro Asn	
170 175 180	
gat gag tgc aaa aaa gcc cac gtc cag aag gtg aca gac ttc atg ctg	630
Asp Glu Cys Lys Lys Ala His Val Gln Lys Val Thr Asp Phe Met Leu	
185 190 195	
tgt gtc gga cac ctg gaa ggt ggc aaa gac acc tgt gtg ggt gat tca	678
Cys Val Gly His Leu Glu Gly Gly Lys Asp Thr Cys Val Gly Asp Ser	
200 205 210	
ggg ggc ccg ctg atg tgt gat ggt gtg ctc caa ggt gtc aca tca tgg	726
Gly Gly Pro Leu Met Cys Asp Gly Val Leu Gln Gly Val Thr Ser Trp	
215 220 225 230	
ggc tac gtc cct tgt ggc acc ccc aat aag cct tct gtc gcc gtc aga	774
Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys Pro Ser Val Ala Val Arg	
235 240 245	
gtg ctg tct tat gtg aag tgg atc gag gac acc ata gcg gag aac tcc	822

Val Leu Ser Tyr Val Lys Trp Ile Glu Asp Thr Ile Ala Glu Asn Ser
250 255 260

tgaacgccca gccctgtccc ctacccccag taaaatcaaa tgtgcatcc

871

<210> 32
<211> 262
<212> PRT
<213> homo sapiens

<400> 32

Met Trp Phe Leu Val Leu Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly
1 5 10 15

Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
20 25 30

Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe
35 40 45

Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala
50 55 60

His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu
65 70 75 80

Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe
85 90 95

Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
100 105 110

Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu
115 120 125

Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr
130 135 140

Glu Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser
145 150 155 160

Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp
165 170 175

Leu Lys Ile Leu Pro Asn Asp Glu Cys Lys Lys Ala His Val Gln Lys
180 185 190

Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp
195 200 205

Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu
210 215 220

Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys
225 230 235 240

Pro Ser Val Ala Val Arg Val Leu Ser Tyr Val Lys Trp Ile Glu Asp
245 250 255

Thr Ile Ala Glu Asn Ser
260

<210> 33
<211> 871
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (37)..(822)

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Met Trp Phe Leu Val Leu
1 5

tgc ctc gcc ctg tcc ctg ggg ggg act ggt gct gcg ccc ccg att cag 102
Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly Ala Ala Pro Ile Gln
10 15 20

tcc cgg att gtg gga ggc tgg gag tgt gag cag cat tcc cag ccc tgg 150
Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Gln His Ser Gln Pro Trp
25 30 35

cag gcg gct ctg tac cat ttc agc act ttc cag tgt ggg ggc atc ctg 198
Gln Ala Ala Leu Tyr His Phe Ser Thr Phe Gln Cys Gly Gly Ile Leu
40 45 50

gtg cac cgc cag tgg gtg ctc aca gct gct cat tgc atc agc gac aat 246
Val His Arg Gln Trp Val Leu Thr Ala Ala His Cys Ile Ser Asp Asn
55 60 65 70

tac cag ctc tgg ctg ggt cgc cac aac ttg ttt gac gac gaa aac aca 294
Tyr Gln Leu Trp Leu Gly Arg His Asn Leu Phe Asp Asp Glu Asn Thr
75 80 85

gcc cag ttt gtt cat gtc agt gag agc ttc cca cac cct ggc ttc aac 342
Ala Gln Phe Val His Val Ser Glu Ser Phe Pro His Pro Gly Phe Asn
90 95 100

atg agc ctc ctg gag aac cac acc cgc caa gca gac gag gac tac agc 390
Met Ser Leu Leu Glu Asn His Thr Arg Gln Ala Asp Glu Asp Tyr Ser
105 110 115

cac gac ctc atg ctg ctc cgc ctg aca gag cct gct gat acc atc aca 438
His Asp Leu Met Leu Leu Arg Leu Thr Glu Pro Ala Asp Thr Ile Thr
120 125 130

gat gct gtg aag gtc gtg gag ttg ccc acc gag gaa ccc gaa gtg ggg 486
Asp Ala Val Lys Val Val Glu Leu Pro Thr Glu Glu Pro Glu Val Gly
135 140 145 150

agc acc tgt ttg gct tcc ggc tgg ggc agc atc gaa cca gag aat ttc 534
Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Asn Phe
155 160 165

tca ttt cca gat gat ctc cag tgt gtg gac ctc aaa atc ctg cct aat 582
Ser Phe Pro Asp Asp Leu Gln Cys Val Asp Leu Lys Ile Leu Pro Asn
170 175 180

gat gag tgc gaa aaa gcc cac gtc cag aag gtg aca gac ttc atg ctg 630
Asp Glu Cys Glu Lys Ala His Val Gln Lys Val Thr Asp Phe Met Leu
185 190 195

tgt gtc gga cac ctg gaa ggt ggc aaa gac acc tgt gtg ggt gat tca 678
Cys Val Gly His Leu Glu Gly Gly Lys Asp Thr Cys Val Gly Asp Ser
200 205 210

ggg ggc ccg ctg atg tgt gat ggt gtg ctc caa ggt gtc aca tca tgg 726
Gly Gly Pro Leu Met Cys Asp Gly Val Leu Gln Gly Val Thr Ser Trp
215 220 225 230

ggc tac gtc cct tgt ggc acc ccc aat aag cct tct gtc gcc gtc aga 774
Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys Pro Ser Val Ala Val Arg
235 240 245

gtg ctg tct tat gtg aag tgg atc gag gac acc ata gcg gag aac tcc 822
Val Leu Ser Tyr Val Lys Trp Ile Glu Asp Thr Ile Ala Glu Asn Ser
250 255 260

tgaacgcccc gccctgtccc ctacccccag taaaatcaaa tgtgcatcc 871

<210> 34
<211> 262
<212> PRT
<213> homo sapiens

<400> 34

Met Trp Phe Leu Val Leu Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly
1 5 10 15

Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
20 25 30

Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe
35 40 45

Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala
50 55 60

His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu
65 70 75 80

Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe
85 90 95

Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
100 105 110

Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu
115 120 125

Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr
130 135 140

Glu Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser
145 150 155 160

Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp
165 170 175

Leu Lys Ile Leu Pro Asn Asp Glu Cys Glu Lys Ala His Val Gln Lys
180 185 190

Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp
195 200 205

Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu
210 215 220

Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys
225 230 235 240

Pro Ser Val Ala Val Arg Val Leu Ser Tyr Val Lys Trp Ile Glu Asp
245 250 255

Thr Ile Ala Glu Asn Ser
260

<210> 35
<211> 871
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (37)..(822)

<400> 35
tcctccacct gctggcccct ggacacctct gtcacc atg tgg ttc ctg gtt ctg 54
Met Trp Phe Leu Val Leu
1 5
tgc ctc gcc ctg tcc ctg ggg ggg act ggt gct gcg ccc ccg att cag 102
Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly Ala Ala Pro Pro Ile Gln
10 15 20
tcc cgg att gtg gga gcc tgg gag tgt gag cag cat tcc cag ccc tgg 150
Ser Arg Ile Val Gly Gly Trp Glu Cys Glu Gln His Ser Gln Pro Trp
25 30 35
cag gcg gct ctg tac cat ttc agc act ttc cag tgt ggg ggc atc ctg 198
Gln Ala Ala Leu Tyr His Phe Ser Thr Phe Gln Cys Gly Gly Ile Leu
40 45 50
gtg cac cgc cag tgg gtg ctc aca gct gct cat tgc atc agc gac aat 246
Val His Arg Gln Trp Val Leu Thr Ala Ala His Cys Ile Ser Asp Asn
55 60 65 70
tac cag ctc tgg ctg ggt cgc cac aac ttg ttt gac gac gaa aac aca 294
Tyr Gln Leu Trp Leu Gly Arg His Asn Leu Phe Asp Asp Glu Asn Thr
75 80 85
gcc cag ttt gtt cat gtc agt gag agc ttc cca cac cct gcc ttc aac 342
Ala Gln Phe Val His Val Ser Glu Ser Phe Pro His Pro Gly Phe Asn
90 95 100
atg agc ctc ctg gag aac cac acc cgc caa gca gac gag gac tac agc 390
Met Ser Leu Leu Glu Asn His Thr Arg Gln Ala Asp Ala Asp Tyr Ser
105 110 115
cac gac ctc atg ctg ctc cgc ctg aca gag cct gct gat acc atc aca 438
His Asp Leu Met Leu Leu Arg Leu Thr Glu Pro Ala Asp Thr Ile Thr
120 125 130
gat gct gtg aag gtc gtg gag ttg ccc acc cag gaa ccc gaa gtg ggg 486
Asp Ala Val Lys Val Val Glu Leu Pro Thr Gln Glu Pro Glu Val Gly

135		140		145		150	
agc acc tgt ttg gct tcc ggc tgg ggc agc atc gaa cca gag aat ttc							534
Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Asn Phe							
	155			160		165	
tca ttt cca gat gat ctc cag tgt gtg gac ctc aaa atc ctg cct aat							582
Ser Phe Pro Asp Asp Leu Gln Cys Val Asp Leu Lys Ile Leu Pro Asn							
	170			175		180	
gat gag tgc aaa aaa gcc cac gtc cag aag gtg aca gac ttc atg ctg							630
Asp Glu Cys Lys Lys Ala His Val Gln Lys Val Thr Asp Phe Met Leu							
	185			190		195	
tgt gtc gga cac ctg gaa ggt ggc aaa gac acc tgt gtg ggt gat tca							678
Cys Val Gly His Leu Glu Gly Gly Lys Asp Thr Cys Val Gly Asp Ser							
	200			205		210	
ggg ggc ccg ctg atg tgt gat ggt gtg ctc caa ggt gtc aca tca tgg							726
Gly Gly Pro Leu Met Cys Asp Gly Val Leu Gln Gly Val Thr Ser Trp							
	215			220		225	230
ggc tac gtc cct tgt ggc acc ccc aat aag cct tct gtc gcc gtc aga							774
Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys Pro Ser Val Ala Val Arg							
	235			240		245	
gtg ctg tct tat gtg aag tgg atc gag gac acc ata gcg gag aac tcc							822
Val Leu Ser Tyr Val Lys Trp Ile Glu Asp Thr Ile Ala Glu Asn Ser							
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20 25 30							
Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe							
35 40 45							
Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala							
50 55 60							
His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu							

65		70		75		80
Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe						
	85			90		95
Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln						
	100			105		110
Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu						
	115			120		125
Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr						
	130			135		140
Gln Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser						
	145			150		155
Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp						
	165			170		175
Leu Lys Ile Leu Pro Asn Asp Glu Cys Lys Lys Ala His Val Gln Lys						
	180			185		190
Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp						
	195			200		205
Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu						
	210			215		220
Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys						
	225			230		235
Pro Ser Val Ala Val Arg Val Leu Ser Tyr Val Lys Trp Ile Glu Asp						
	245			250		255
Thr Ile Ala Glu Asn Ser						
	260					

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<210> 38
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<400> 38
agaacagtct agtggtaca 19

<210> 39
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<400> 39
ctcaccaccc tcccccaag 19

<210> 40
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<400> 40
aggcctcagt ccaagctga 19

<210> 41
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<400> 41
cgggccccag ccctcactc 19

<210> 42
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<212> DNA
<213> homo sapiens

<400> 42
taataaaaaga ggggtggcc 19

<210> 43
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<212> DNA
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<400> 43
aaaagcagcg aaacccttt 19

<210> 44
 <211> 18
 <212> DNA
 <213> homo sapiens

<400> 44
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18

<210> 45
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 35 40 45
 Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
 50 55 60
 Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
 65 70 75 80
 Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
 85 90 95
 Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
 100 105 110
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 Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
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Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
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Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
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Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Xaa Leu
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Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
                      195                      200                      205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
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Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
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Xaa Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
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Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
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Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
275                      280                      285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
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Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Xaa Leu Phe Arg
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Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
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 agaaggacc tgagccccag gcgccagcca caggactctg ctgcagaggg gggttgtgta 180
 cagatagtag gccttacgcc tagcttcgaa atg gat aac gtc ctc ccg gtg gac 234
 Met Asp Asn Val Leu Pro Val Asp
 1 5
 tca gac ctc tcc cca aac atc tcc act aac acc tgc gaa ccc aat cag 282
 Ser Asp Leu Ser Pro Asn Ile Ser Thr Asn Thr Ser Glu Pro Asn Gln
 10 15 20
 ttc gtg caa cca gcc tgg caa att gtc ctt tgg gca gct gcc tac acg 330
 Phe Val Gln Pro Ala Trp Gln Ile Val Leu Trp Ala Ala Ala Tyr Thr
 25 30 35 40
 gtc att gtg gtg acc tct gtg gtg ggc aac gtg gta gtg atg tgg atc 378
 Val Ile Val Val Thr Ser Val Val Gly Asn Val Val Val Met Trp Ile
 45 50 55
 atc tta gcc cac aaa aga atg agg aca gtg acg aac tat ttt ctg gtg 426
 Ile Leu Ala His Lys Arg Met Arg Thr Val Thr Asn Tyr Phe Leu Val
 60 65 70
 aac ctg gcc ttc gcg gag gcc tcc atg gct gca ttc aat aca gtg gtg 474
 Asn Leu Ala Phe Ala Glu Ala Ser Met Ala Ala Phe Asn Thr Val Val
 75 80 85
 aac ttc acc tat gct gtc cac aac gaa tgg tac tac ggc ctg ttc tac 522
 Asn Phe Thr Tyr Ala Val His Asn Glu Trp Tyr Tyr Gly Leu Phe Tyr
 90 95 100
 tgc aag ttc cac aac ttc ttn ccc atc gcc gct gtc ttc gcc agt atc 570
 Cys Lys Phe His Asn Phe Xaa Pro Ile Ala Ala Val Phe Ala Ser Ile
 105 110 115 120
 tac tcc atg acg gct gtg gcc ttt gat agg tac atg gcc atc ata cat 618
 Tyr Ser Met Thr Ala Val Ala Phe Asp Arg Tyr Met Ala Ile Ile His
 125 130 135
 ccc ctc cag ccc cgg ctg tca gcc aca gcc acc aaa gtg gtc atc tgt 666

Pro Leu Gln Pro Arg Leu Ser Ala Thr Ala Thr Lys Val Val Ile Cys	
140 145 150	
gtc atn tgg gtc ctg gct ctc ctg gcc ttc ccc cag ggc tac tac	714
Val Xaa Trp Val Leu Ala Leu Leu Ala Phe Pro Gln Gly Tyr Tyr	
155 160 165	
tca acc aca gag acc atg ccc agc aga gtc gtg tgc atg atc gaa tgg	762
Ser Thr Thr Glu Thr Met Pro Ser Arg Val Val Cys Met Ile Glu Trp	
170 175 180	
cca gag cat ccg aac aag att tat gag aaa gtg tac cac atc tgt gtg	810
Pro Glu His Pro Asn Lys Ile Tyr Glu Lys Val Tyr His Ile Cys Val	
185 190 195	
act gtg ctg atc tac ttc ctc ccc ctg ctg gtg att ggc tat gca tac	858
Thr Val Leu Ile Tyr Phe Leu Pro Leu Leu Val Ile Gly Tyr Ala Tyr	
205 210 215	
acc gta gtg gga atc aca cta tgg gcc agt gag atc ccc ggg gac tcc	906
Thr Val Val Gly Ile Thr Leu Trp Ala Ser Glu Ile Pro Gly Asp Ser	
220 225 230	
tct gac cgc tac cac gag caa gtc tct gcc aag cgc aag gtg gtc aaa	954
Ser Asp Arg Tyr His Glu Gln Val Ser Ala Lys Arg Lys Val Val Lys	
235 240 245	
atg atg att gtc gtg gtg tgc acc ttc gcc atc tgc tgg ctg ccc ttc	1002
Met Met Ile Val Val Val Cys Thr Phe Ala Ile Cys Trp Leu Pro Phe	
250 255 260	
cac atc ttc ttc ctc ctg ccc tac atc aac cca gat ctc tac ctg aag	1050
His Ile Phe Phe Leu Leu Pro Tyr Ile Asn Pro Asp Leu Tyr Leu Lys	
265 270 275	
aag ttt atc cag cag gtc tac ctg gcc atc atg tgg ctg gcc atg agc	1098
Lys Phe Ile Gln Gln Val Tyr Leu Ala Ile Met Trp Leu Ala Met Ser	
285 290 295	
tcc acc atg tac aac ccc atc atc tac tgc tgc ctc aat gac agg ttc	1146
Ser Thr Met Tyr Asn Pro Ile Ile Tyr Cys Cys Leu Asn Asp Arg Phe	
300 305 310	
cgt ctg ggc ttc aag cat gcc ttc cgg tgc tgc ccc ttc atc agc gcc	1194
Arg Leu Gly Phe Lys His Ala Phe Arg Cys Cys Pro Phe Ile Ser Ala	
315 320 325	
ggc gac tat gag ggg ctg gaa atg aaa tcc acc cgg tat ctc cag acc	1242
Gly Asp Tyr Glu Gly Leu Glu Met Lys Ser Thr Arg Tyr Leu Gln Thr	
330 335 340	
cag ggc agt gtg tac aaa gtc agc cgc ctg gag acc acc atc tcc aca	1290
Gln Gly Ser Val Tyr Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr	
345 350 355	
gtg gtg ggg gcc cac gag gag gag cca gag gac ggc ccc aag gcc aca	1338
Val Val Gly Ala His Glu Glu Glu Pro Glu Asp Gly Pro Lys Ala Thr	

ccc tcn tcc ctg gac ctg acc tcc aac tgc tct tca cga agt gac tcc	1386
Pro Xaa Ser Leu Asp Leu Thr Ser Asn Cys Ser Ser Arg Ser Asp Ser	
380 385 390	
aag acc atg aca gag agc ttc agc ttc tcc tcc aat gtg ctc tcc	1431
Lys Thr Met Thr Glu Ser Phe Ser Phe Ser Ser Asn Val Leu Ser	
395 400 405	
tagggccacag ggccctttggc aggtgcagcc cccactgcct ttgacctgcc tcccttcctg	1491
catggaaatt cccctcatct ggaaccatca gaaacaccct cacactggga cttgcaaaaa	1551
gggtcagtat gggttaggga aaacattcca tcccttgagtc aaaaaatctc aattcttccc	1611
tatctttgcc accctcatgc tgtgtgactc aaaccaaact actgaacttt gctgagcctg	1671
taaaataaaa ggtcggacca gcttttcctc aagagcccaa tgcattccat ttctggaagt	1731
gactttggct gcatgcgagt gctcatttca ggatg	1766
<210> 292	
<211> 407	
<212> PRT	
<213> homo sapiens	
<220>	
<221> misc_feature	
<222> (543)..(543)	
<223> wherein N is either a "T" or a "C".	
<220>	
<221> misc_feature	
<222> (672)..(672)	
<223> wherein N is either a "C" or an "A".	
<220>	
<221> misc_feature	
<222> (1344)..(1344)	
<223> wherein N is either a "G" or an "A".	
<400> 292	
Met Asp Asn Val Leu Pro Val Asp Ser Asp Leu Ser Pro Asn Ile Ser	
1 5 10 15	
Thr Asn Thr Ser Glu Pro Asn Gln Phe Val Gln Pro Ala Trp Gln Ile	
20 25 30	
Val Leu Trp Ala Ala Ala Tyr Thr Val Ile Val Val Thr Ser Val Val	
35 40 45	

Gly Asn Val Val Val Met Trp Ile Ile Leu Ala His Lys Arg Met Arg
50 55 60

Thr Val Thr Asn Tyr Phe Leu Val Asn Leu Ala Phe Ala Glu Ala Ser
65 70 75 80

Met Ala Ala Phe Asn Thr Val Val Asn Phe Thr Tyr Ala Val His Asn
85 90 95

Glu Trp Tyr Tyr Gly Leu Phe Tyr Cys Lys Phe His Asn Phe Xaa Pro
100 105 110

Ile Ala Ala Val Phe Ala Ser Ile Tyr Ser Met Thr Ala Val Ala Phe
115 120 125

Asp Arg Tyr Met Ala Ile Ile His Pro Leu Gln Pro Arg Leu Ser Ala
130 135 140

Thr Ala Thr Lys Val Val Ile Cys Val Xaa Trp Val Leu Ala Leu Leu
145 150 155 160

Leu Ala Phe Pro Gln Gly Tyr Tyr Ser Thr Thr Glu Thr Met Pro Ser
165 170 175

Arg Val Val Cys Met Ile Glu Trp Pro Glu His Pro Asn Lys Ile Tyr
180 185 190

Glu Lys Val Tyr His Ile Cys Val Thr Val Leu Ile Tyr Phe Leu Pro
195 200 205

Leu Leu Val Ile Gly Tyr Ala Tyr Thr Val Val Gly Ile Thr Leu Trp
210 215 220

Ala Ser Glu Ile Pro Gly Asp Ser Ser Asp Arg Tyr His Glu Gln Val
225 230 235 240

Ser Ala Lys Arg Lys Val Val Lys Met Met Ile Val Val Val Cys Thr
245 250 255

Phe Ala Ile Cys Trp Leu Pro Phe His Ile Phe Phe Leu Leu Pro Tyr
260 265 270

Ile Asn Pro Asp Leu Tyr Leu Lys Lys Phe Ile Gln Gln Val Tyr Leu

275

280

285

Ala Ile Met Trp Leu Ala Met Ser Ser Thr Met Tyr Asn Pro Ile Ile
 290 295 300

Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe Lys His Ala Phe
 305 310 315 320

Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu Gly Leu Glu Met
 325 330 335

Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Ser Val Tyr Lys Val Ser
 340 345 350

Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His Glu Glu Glu
 355 360 365

Pro Glu Asp Gly Pro Lys Ala Thr Pro Xaa Ser Leu Asp Leu Thr Ser
 370 375 380

Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr Glu Ser Phe Ser
 385 390 395 400

Phe Ser Ser Asn Val Leu Ser
 405

<210> 293
 <211> 1826
 <212> DNA
 <213> homo sapiens

<220>
 <221> misc_feature
 <222> (1278)..(1278)
 <223> wherein N is either a "C" or a "T".

<220>
 <221> misc_feature
 <222> (227)..(227)
 <223> wherein N is either a "T" or a "C".

<220>
 <221> misc_feature
 <222> (536)..(536)
 <223> wherein N is either a "C" or a "G".

<220>
 <221> misc_feature
 <222> (1498)..(1498)
 <223> wherein N is either a "G" or an "A".

<400> 293
 agtctgcact ggagctgcct ggtgaccaga agtttggagt ccgctgacgt cgccgcccag 60
 atggcctcca ggtgacctc gctgacctc ctgctgctgc tgctggctgg ggatagagcc 120
 tcctcaaatc caaatgtac cagctccagc tcccaggatc cagagagttt gcaagacaga 180
 ggcgaaggga aggtcgcaac aacagttatc tccaagatgc tattecgtga acccatcctg 240
 gaggtttcca gcttgccgac aaccaactca acaaccaatt cagccacca aataacagct 300
 aataaccactg atgaaccac cacacaacc accacagagc ccaccacca acccaccatc 360
 caaccacccc aaccaactac ccagctccca acagattctc ctaccagcc cactactggg 420
 tcctctctgc caggacctg tactctctgc tctgacttgg agagtcattc aacagagggc 480
 gtgttggggg atgctttggt agatttctcc ctgaagctct accacgcctt ctcagnaatg 540
 aagaaggtgg agaccaacat ggccctttcc ccattcagca tcgccagcct ccttaccag 600
 gtctctctgc gggctgggca gaacacaaa acaaacctgg agagcattct ctcttacc 660
 aaggacttca cctgtgtcca ccaggccctg aagggttcca cgaccaaagg tgtaacctca 720
 gtctctcaga tcttccacag ccagacctg gccataaggg acacctttgt gaatgcctct 780
 cggacctgtt acagcagcag cccagagatc ctaagcaaca acagtgcgc caacttggag 840
 ctcatcaaca cctgggtggc caagaacacc aacaacaaga tcagccggct gctagacagt 900
 ctgcccctcg ataccgcct tgtctctctc aatgctatct acctgagtgc caagtggag 960
 acaacatttg atcccaagaa aaccagaatg gaacctttc acttcaaaaa ctcagttata 1020
 aaagtgccta tgatgaatag caagaagtac cctgtggccc atttcattga ccaaacttgg 1080
 aaagccaagg tggggcagct gcagctctcc cacaatatga gtttgggtgat cctggtaccc 1140
 cagaacctga aacatcgtct tgaagacatg gaacagctc tcagcccttc tgttttcaag 1200
 gccatcatgg agaaactgga gatgtccaag ttccagccca ctctcctaac actacccgc 1260
 atcaaagtga cgaccagnca ggatatgtct tcaatcatgg agaaattgga attcttcgat 1320
 ttttcttatg accttaacct gtgtgggctg acagaggacc cagatcttca ggtttctgag 1380
 atgcagcacc agacagtgtc ggaactgaca gagactgggg tggagggggc tgcagcctcc 1440
 gccatctctg tggcccgcac cctgtgggtc tttgaagtgc agcagccctt cctcttctg 1500

ctctggggacc agcagcacaa gttccctgtc ttcattggggc gagtatatga cccaggggcc 1560
 tgagacctgc aggatcaggt tagggcgagc gctacctctc cagcctcagc tctcagttgc 1620
 agccctgtgt ctgcctgcct ggacttgccc ctgccacctc ctgcctcagg tgctcgtat 1680
 ccaccaaag ggctcctgag ggtctgggca agggacctgc ttctattagc cttctccat 1740
 ggccctgcca tgctctccaa accacttttt gcagctttct ctagtccaag ttcaccagac 1800
 tctataaata aaacctgaca gaccat 1826

<210> 294
 <211> 500
 <212> PRT
 <213> homo sapiens

<220>
 <221> VARIANT
 <222> (56)..(56)
 <223> wherein Xaa is either "Val" or "Ala".

<220>
 <221> VARIANT
 <222> (159)..(159)
 <223> wherein Xaa is either "Ala" or "Gly".

<220>
 <221> VARIANT
 <222> (480)..(480)
 <223> wherein Xaa is either "Val" or "Met".

<400> 294

Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Ala
 1 5 10 15

Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln
 20 25 30

Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr
 35 40 45

Val Ile Ser Lys Met Leu Phe Xaa Glu Pro Ile Leu Glu Val Ser Ser
 50 55 60

Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala
 65 70 75 80

Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr
 85 90 95

<221> misc_feature
 <222> (348)..(348)
 <223> wherein N is either a "C" or a "T".

<220>
 <221> misc_feature
 <222> (462)..(462)
 <223> wherein N is either a "G" or an "A".

<220>
 <221> misc_feature
 <222> (577)..(577)
 <223> wherein N is either a "C" or a "G".

<220>
 <221> misc_feature
 <222> (705)..(705)
 <223> wherein N is either a "G" or an "A".

<400> 289
 ctgtgcatgg catcatctgg gccccctcta gagctccaat cctccaacca gagccagctc 60
 ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctggggacct gctgcacaga 120
 gtgctgccna catttatcat ctccatctgt ttctctggcc tcttagggaa cctttttgtc 180
 ctgttggtct tctctctgcc cgggcggcaa ctgaacgtgg cagaaatcta cctggccaac 240
 ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300
 aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaangg ggtcatcaag 360
 gccaatttgt tcatcagcat ctctctggtg gtggccatca gccaggaccg ctaccgcgtg 420
 ctggtgcacc ctatggccag cgggaaggcag cagcggcgga gncaggcccg ggtcacctgc 480
 gtgctcatct ggggttgagg gggcctcttg agcateccca cattctctgt gcgatccatc 540
 caagccgtcc cagatctgaa cateaccgcc tgcattctgc tctctcccca tgaggcctgg 600
 cactttgcaa ggatttgga gttaaatatt ctgggtttcc tctaccact gctgcgcatc 660
 gtctcttcta actaaccacat cctggcctcc ctgcgaacgc gggangaggt cagcaggaca 720
 agagtgcngg ggccgaagga tagcaagacc acagcgctga tctctacgct cgtggttgcc 780
 ttctctggtc gctgggcccc ttaccacttc ttgccttcc tggaaattctt attccaggtg 840
 caagcagtc caggctgctt ttgggaggac ttcatlgacc tgggcctgca attggccaac 900
 ttctttgctc tcaactaacg ctcccgaat ccagtaattt atgtctttgt gggcngctc 960
 ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020

Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp
 100 105 110
 Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr
 115 120 125
 Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp
 130 135 140
 Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Xaa Met
 145 150 155 160
 Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
 165 170 175
 Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Gln Asn Thr Lys Thr Asn
 180 185 190
 Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
 195 200 205
 Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
 210 215 220
 Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
 225 230 235 240
 Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
 245 250 255
 Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
 260 265 270
 Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
 275 280 285
 Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
 290 295 300
 Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
 305 310 315 320
 Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
 325 330 335
 Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn
 340 345 350
 Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu
 355 360 365
 Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu
 370 375 380
 Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg
 385 390 395 400

Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu
405 410 415

Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu
420 425 430

Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu
435 440 445

Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ser Ala Ile Ser Val
450 455 460

Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Xaa
465 470 475 480

Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr
485 490 495

Asp Pro Arg Ala
500

<210> 295
<211> 871
<212> DNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (592)..(592)
<223> wherein N is either an "A" or a "G".

<220>
<221> misc_feature
<222> (469)..(469)
<223> wherein N is either a "G" or a "C".

<400> 295
tctccacct gctggccctt ggacacctt gtcaccatgt ggttctctggt tctgtgcctc 60

gcctgtccc tgggggggac tgggtgctgcg cccccgattc agtcccggat tgtgggaggg 120

tgggagtggt agcagcattc ccagccctgg caggcggtct tgtaccattt cagcactttc 180

cagtgtgggg gcatctcgtt gcaccgccag tgggtgctca cagctgtctca ttgcatcagc 240

gacaattacc agctctggct gggtcgccac aactgtgttg acgacgaaaa cacagcccag 300

ttgtttcatg tcagtgtgag cttccacacac cctgggtctca acatgagcct cctggagaac 360

cacacccgcc aagcagacga ggactacagc cagcactctc tgctgtctcg cctgacagag 420

cctgtctgata ccatcacaga tgctgtgaag gtctgtgaggt tgcccaccna ggaacccgaa 480

gtggggagca cctgtttggc ttccggctgg ggcagcatcg aaccagagaa ttctctcatt 540

ccagatgac tccagtgtgt ggacctcaaa atcctgccta atgatgagt cnaaaaagcc 600
 cactgccaga aggtgacaga cttcatgctg tgtgtcggac acctggaagg tggcaaaagac 660
 acctgtgtgg gtgattcagg gggcccgtg atgtgtgatg gtgtgtcca aggtgtcaca 720
 tcatggggct acgtcccttg tggcaccccc aataagcett ctgtgcgcgt cagagtgtgtg 780
 tcttatgtga agtggatcga ggacaccata gcggagaact cctgaacgcc cagccctgtc 840
 ccctaccccc agtaaaatca aatgtgcac c 871

<210> 296
 <211> 262
 <212> PRT
 <213> homo sapiens

<220>
 <221> VARIANT
 <222> (145)..(145)
 <223> wherein Xaa is either "Glu" or "Asn".

<220>
 <221> VARIANT
 <222> (186)..(186)
 <223> wherein Xaa is either "Lys" or "Glu".

<400> 296

Met Trp Phe Leu Val Leu Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly
 1 5 10 15
 Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
 20 25 30
 Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe
 35 40 45
 Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala
 50 55 60
 His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu
 65 70 75 80
 Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe
 85 90 95
 Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
 100 105 110
 Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu
 115 120 125
 Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr

130

135

140

Xaa Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser
145 150 155 160

Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp
165 170 175

Leu Lys Ile Leu Pro Asn Asp Glu Cys Xaa Lys Ala His Val Gln Lys
180 185 190

Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp
195 200 205

Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu
210 215 220

Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys
225 230 235 240

Pro Ser Val Ala Val Arg Val Leu Ser Tyr Val Lys Trp Ile Glu Asp
245 250 255

Thr Ile Ala Asn Ser
260

<210> 297

<211> 21

<212> DNA

<213> homo sapiens

<400> 297

cagcccaggc atcttaatatct a

21

<210> 298

<211> 20

<212> DNA

<213> homo sapiens

<400> 298

agtgctcctt ccttccttc

20

<210> 299

<211> 21

<212> DNA

<213> homo sapiens

<400> 299

tagctgtcctt cttcctttcg c

21

<210> 300

<211> 21

<212> DNA

<213> homo sapiens

<400> 300
tagctgtctt cttcctttcg c 21

<210> 301
<211> 21
<212> DNA
<213> homo sapiens

<400> 301
tgattgagac cagctgttgt g 21

<210> 302
<211> 18
<212> DNA
<213> homo sapiens

<400> 302
ccagcgtggg catacatg 18

<210> 303
<211> 18
<212> DNA
<213> homo sapiens

<400> 303
ccagcgtggg catacatg 18

<210> 304
<211> 21
<212> DNA
<213> homo sapiens

<400> 304
cttcctttga cctcaggaa c 21

<210> 305
<211> 21
<212> DNA
<213> homo sapiens

<400> 305
cttcctttga cctcaggaa c 21

<210> 306
<211> 18
<212> DNA
<213> homo sapiens

<400> 306
ccagcgtggg catacatg 18

<210> 307
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 307
 taaatgacag gtcagggtt g 21

<210> 308
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 308
 taaatgacag gtcagggtt g 21

<210> 309
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 309
 taaatgacag gtcagggtt g 21

<210> 310
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 310
 tgattgagac cagctgttgt g 21

<210> 311
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 311
 tgattgagac cagctgttgt g 21

<210> 312
 <211> 22
 <212> DNA
 <213> homo sapiens

<400> 312
 ggcccatgtc attaatgagt ac 22

<210> 313

<211> 21
 <212> DNA
 <213> homo sapiens

 <400> 313
 ccctcttctt aggcaccact c 21

 <210> 314
 <211> 21
 <212> DNA
 <213> homo sapiens

 <400> 314
 ccctcttctt aggcaccact c 21

 <210> 315
 <211> 21
 <212> DNA
 <213> homo sapiens

 <400> 315
 tagctgtctt cttctcttgc c 21

 <210> 316
 <211> 21
 <212> DNA
 <213> homo sapiens

 <400> 316
 ggactatggt gacagctgga g 21

 <210> 317
 <211> 21
 <212> DNA
 <213> homo sapiens

 <400> 317
 ggactatggt gacagctgga g 21

 <210> 318
 <211> 21
 <212> DNA
 <213> homo sapiens

 <400> 318
 gaggctccag actctctgt t 21

 <210> 319
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 319
gaggctccag actctctgt t 21

<210> 320
<211> 21
<212> DNA
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 tgtcagtggc ctgaaatatt c 21

 <210> 490
 <211> 20
 <212> DNA
 <213> homo sapiens

<400> 490	
agaggtcaga gctgccttcc	20
<210> 491	
<211> 21	
<212> DNA	
<213> homo sapiens	
<400> 491	
taaacaagca tcccaggtga c	21
<210> 492	
<211> 21	
<212> DNA	
<213> homo sapiens	
<400> 492	
taaacaagca tcccaggtga c	21
<210> 493	
<211> 21	
<212> DNA	
<213> homo sapiens	
<400> 493	
aagaaggga ctcactgcac a	21
<210> 494	
<211> 21	
<212> DNA	
<213> homo sapiens	
<400> 494	
aagaaggga ctcactgcac a	21
<210> 495	
<211> 21	
<212> DNA	
<213> homo sapiens	
<400> 495	
taaacaagca tcccaggtga c	21
<210> 496	
<211> 21	
<212> DNA	
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<400> 496	
gcaactccct actccacact g	21

<210> 497
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 <213> homo sapiens

<400> 497
 gcaactccct actccacact g 21

<210> 498
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<400> 498
 gcaactccct actccacact g 21

<210> 499
 <211> 20
 <212> DNA
 <213> homo sapiens

<400> 499
 agaggtcaga gctgccttcc 20

<210> 500
 <211> 20
 <212> DNA
 <213> homo sapiens

<400> 500
 agaggtcaga gctgccttcc 20

<210> 501
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 501
 cttacccttc ttgggtccca c 21

<210> 502
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 502
 agctgggtaa ccttgggtag a 21

<210> 503

<211> 21
 <212> DNA
 <213> homo sapiens

<400> 503
 agctgggtaa ccttgggtag a 21

<210> 504
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 504
 tgtcagtggc ctgaaatata c 21

<210> 505
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 505
 tgggaccttc tccatagggt c 21

<210> 506
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 506
 tgggaccttc tccatagggt c 21

<210> 507
 <211> 20
 <212> DNA
 <213> homo sapiens

<400> 507
 gggtgatgtt tcatgccctg 20

<210> 508
 <211> 20
 <212> DNA
 <213> homo sapiens

<400> 508
 gggtgatgtt tcatgccctg 20

<210> 509
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 509
tcaatgctgt ttttaattccg c

21

<210> 510
<211> 21
<212> DNA
<213> homo sapiens

<400> 510
atgaacaaat tggccttgat g

21

<210> 511
<211> 20
<212> DNA
<213> homo sapiens

<400> 511
aggacccatt cttcttgga

20

<210> 512
<211> 21
<212> DNA
<213> homo sapiens

<400> 512
ggatcagatg aacccaggag t

21

<210> 513
<211> 21
<212> DNA
<213> homo sapiens

<400> 513
tgggtgttc atgcaatttc t

21

<210> 514
<211> 19
<212> DNA
<213> homo sapiens

<400> 514
ctttgggatt cctccctt

19

<210> 515
<211> 19
<212> DNA
<213> homo sapiens

<400> 515
ctttgggatt cctccctt

19

<210> 516
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 <212> DNA
 <213> homo sapiens

<400> 516
 ccgaggttct ctggagaaaa a 21

<210> 517
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 517
 ccgaggttct ctggagaaaa a 21

<210> 518
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 518
 ccgaggttct ctggagaaaa a 21

<210> 519
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 519
 ccgaggttct ctggagaaaa a 21

<210> 520
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 520
 ggtccacttg tctctcttct t 21

<210> 521
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 521
 cagaaagctg ttcgacgaga c 21

<210> 522

<211> 21
 <212> DNA
 <213> homo sapiens

 <400> 522
 cagaaagctg ttcgacgaga c 21

 <210> 523
 <211> 21
 <212> DNA
 <213> homo sapiens

 <400> 523
 cagaaagctg ttcgacgaga c 21

 <210> 524
 <211> 21
 <212> DNA
 <213> homo sapiens

 <400> 524
 tggaggaaga aaacaggtga a 21

 <210> 525
 <211> 21
 <212> DNA
 <213> homo sapiens

 <400> 525
 tggaggaaga aaacaggtga a 21

 <210> 526
 <211> 21
 <212> DNA
 <213> homo sapiens

 <400> 526
 tggaggaaga aaacaggtga a 21

 <210> 527
 <211> 21
 <212> DNA
 <213> homo sapiens

 <400> 527
 acacagtagg tgctcattgg c 21

 <210> 528
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 528
tggatgaggt ttttgcata g c 21

<210> 529
<211> 21
<212> DNA
<213> homo sapiens

<400> 529
tggatgaggt ttttgcata g c 21

<210> 530
<211> 21
<212> DNA
<213> homo sapiens

<400> 530
ttaccgcaag agagatgctg t 21

<210> 531
<211> 21
<212> DNA
<213> homo sapiens

<400> 531
tggcaggaaa aatatggaat c 21

<210> 532
<211> 21
<212> DNA
<213> homo sapiens

<400> 532
gtagctgcc aaccttgact g 21

<210> 533
<211> 21
<212> DNA
<213> homo sapiens

<400> 533
gagagcttca gcttctcctc c 21

<210> 534
<211> 21
<212> DNA
<213> homo sapiens

<400> 534
gagagcttca gcttctcctc c 21

<210> 535
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 535
 gagagcttca gcttctcttc c 21

<210> 536
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 536
 aggggtcacct cttcatctgc t 21

<210> 537
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 537
 tctgcagtcc atccctgata c 21

<210> 538
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 538
 accccaaaat gatgggacta c 21

<210> 539
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 539
 cctgggagta accctaagct g 21

<210> 540
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 540
 atctgttggg agctgggtag t 21

<210> 541

<211> 21
 <212> DNA
 <213> homo sapiens

<400> 541
 gtccaacaaa tgacctggag a 21

<210> 542
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 542
 gagctgaggc tggagaggta g 21

<210> 543
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 543
 cctcaccaca caggtgtctt t 21

<210> 544
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 544
 cctcaccaca caggtgtctt t 21

<210> 545
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 545
 cctcaccaca caggtgtctt t 21

<210> 546
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 546
 cctcaccaca caggtgtctt t 21

<210> 547
 <211> 21
 <212> DNA
 <213> homo sapiens

<400> 547
gtgcaccaca tctggaaaga t 21

<210> 548
<211> 21
<212> DNA
<213> homo sapiens

<400> 548
gtgcaccaca tctggaaaga t 21

<210> 549
<211> 24
<212> DNA
<213> bacteriophage m13

<400> 549
agcggataac aatttcacac agga 24

<210> 550
<211> 21
<212> DNA
<213> homo sapiens

<400> 550
agctcttcag gaccaaggtc t 21

<210> 551
<211> 24
<212> DNA
<213> bacteriophage m13

<400> 551
cgccagggtt ttcccagtca cgac 24

<210> 552
<211> 20
<212> DNA
<213> homo sapiens

<400> 552
ggcccacaaa gacataaatt 20

<210> 553
<211> 8
<212> PRT
<213> Bacteriophage T7

<400> 553

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 554
<211> 733
<212> DNA
<213> homo sapiens

<400> 554
gggatccgga gcccaaatct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60
aattcgaggg tgcaccgtca gtcttctctt tccccccaaa acccaaggac accctcatga 120
tctcccgga ccttgaggto acatgcgtgg tgggtggagt aagccacgaa gacctgagg 180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagcccgagg 240
aggagcagta caacagcagc taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtac aagtgcagg tctccaacaa agcctccca accccatcg 360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaagccttct 480
atccaagcga catgcgcgtg gagggtggga gcaatgggca gccggagaa aactacaaga 540
ccacgcctcc cgtgctggac tccgacggct ccttctctct ctacagcaag ctcaccgtgg 600
acaagagcag gtggcagcag ggggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660
acaaccacta cagcgagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
gactctagag gat 733

<210> 555
<211> 1082
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (348)..(348)
<223> wherein N is either a "C" or a "T".

<400> 555
ctgtgcattg catcatctg gccccctcta gagctccaat cctccaacca gagccagctc 60
ttccctcaaa atgctacggc ctgtgacaat gctcagaag cctgggacct gctgcacaga 120
gtgctgcga catttateat ctccatctgt ttcttcggcc tctaggagaa cetttttgtc 180
ctgttggtct tctcctgcc ccggcggcaa ctgaacgtgg cagaaatcta cctggccaac 240
ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300

aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaatgg ggtcatcaag 360
gccaaattgt tcatcagcat cttcctgggtg gtggccatca gccaggaccg ctaccgcgtg 420
ctgggtgacc ctatggccag cggaaggcag cagcggcgga gccaggcccg ggtcacctgc 480
gtgtctatct ggggttgagg gggcctcttg agcatcccca cattctctgt gcgatccatc 540
caagccgtcc cagatctgaa catcacccgc tgcctcctgc tcctccccc tgaggcctgg 600
cactttgcaa ggattgtgga gttaaatatt ctgggtttcc tcctaccact ggctcgatc 660
gtcttcttca actaccacat cctggcctcc ctgcgaacgc gggaggaggt cagcaggaca 720
agagtgcggg ggccgaagga tagcaagacc acagcgctga tcctcacgct cgtggttgcc 780
ttcctggtct gctgggcccc ttaccacttc ttgccttcc tggaattctt attccaggtg 840
caagcagtc caggctgctt ttgggaggac ttcatcgacc tgggcctgca attggccaac 900
ttctttgct tcaactaacg ctccctgaat ccagtaattt atgtctttgt gggcgggctc 960
ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020
tcttcatccc ataggaaaa aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080
cc 1082

<210> 556

<211> 353

<212> PRT

<213> Homo sapiens

<400> 556

Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser
1 5 10 15
Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
20 25 30
Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys
35 40 45
Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
50 55 60
Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
65 70 75 80
Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
85 90 95
Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
100 105 110

```

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
    115                                120
Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
    130                                135                                140
Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
    145                                150                                155                                160
Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
    165                                170                                175
Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
    180                                185                                190
Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
    195                                200
Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
    210                                215                                220
Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
    225                                230                                235                                240
Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
    245                                250                                255
Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
    260                                265                                270
Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
    275                                280                                285
Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
    290                                295                                300
Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
    305                                310                                315                                320
Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
    325                                330                                335
Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
    340                                345                                350

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Asn

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<210> 557
<211> 1082
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (462)..(462)

```

<223> wherein N is either a "G" or an "A".

<400> 557
ctgtgcacgg catcaccctg gcccccctta gagctccaat cctccaacca gagccagctc 60
ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120
gtgctgccga catttatcat ctccatctgt ttcttcggcc tcctagggaa cctttttgtc 180
ctgttggtct tcctcctgcc ccggcgggcaa ctgaacgtgg cagaaatcta cctggccaac 240
ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300
aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaacgg ggtcatcaag 360
gccaatattgt tcatcagcat ctctcctggtg gtggccatca gccaggaccg ctaccgcgtg 420
ctggtgcacc ctatggccag cgggaaggcag cagcggcgga gacaggcccg ggtcacctgc 480
gtgctcatct ggggttggtgg gggcctcttg agcatcccca cattcctgct gcgaccatc 540
caagccgtcc cagatctgaa catcacgcgc tgcactctgc tctccccca tgggcctggt 600
cactttgcga ggatttgga gttaaatatt ctgggtttcc tctaccact ggctgcgac 660
gtcttttca actaccacat cctggcctcc ctgcgaacgc gggaggagggt cagcaggaca 720
agagtgcggg ggccgaagga tagcaagacc acagcgctga tcctcacgct cgtggttgcc 780
ttctcgtct gctgggcccc ttaccacttc tttgccttcc tgggaattctt attccagggt 840
caagcagtcc gagcgtgctt ttgggaggac ttcattgacc tgggcctgca attggccaac 900
ttctttgct tcaactaacag ctccctgaat ccagtaattt atgtctttgt gggccggctc 960
ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020
tcttcacccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080
cc 1082

<210> 558
<211> 353
<212> PRT
<213> Homo sapiens

<400> 558
Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser
1 5 10 15
Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
20 25 30
Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys

35					40					45					
Phe	Phe	Gly	Leu	Leu	Gly	Asn	Leu	Phe	Val	Leu	Leu	Val	Phe	Leu	Leu
50						55					60				
Pro	Arg	Arg	Gln	Leu	Asn	Val	Ala	Glu	Ile	Tyr	Leu	Ala	Asn	Leu	Ala
65					70					75				80	
Ala	Ser	Asp	Leu	Val	Phe	Val	Leu	Gly	Leu	Pro	Phe	Trp	Ala	Glu	Asn
			85						90					95	
Ile	Trp	Asn	Gln	Phe	Asn	Trp	Pro	Phe	Gly	Ala	Leu	Leu	Cys	Arg	Val
			100						105				110		
Ile	Asn	Gly	Val	Ile	Lys	Ala	Asn	Leu	Phe	Ile	Ser	Ile	Phe	Leu	Val
			115					120					125		
Val	Ala	Ile	Ser	Gln	Asp	Arg	Tyr	Arg	Val	Leu	Val	His	Pro	Met	Ala
			130				135					140			
Ser	Gly	Arg	Gln	Gln	Arg	Arg	Arg	Gln	Ala	Arg	Val	Thr	Cys	Val	Leu
145						150					155			160	
Ile	Trp	Val	Val	Gly	Gly	Leu	Leu	Ser	Ile	Pro	Thr	Phe	Leu	Leu	Arg
				165					170					175	
Ser	Ile	Gln	Ala	Val	Pro	Asp	Leu	Asn	Ile	Thr	Ala	Cys	Ile	Leu	Leu
			180					185					190		
Leu	Pro	His	Glu	Ala	Trp	His	Phe	Ala	Arg	Ile	Val	Glu	Leu	Asn	Ile
			195				200					205			
Leu	Gly	Phe	Leu	Leu	Pro	Leu	Ala	Ala	Ile	Val	Phe	Phe	Asn	Tyr	His
			210				215					220			
Ile	Leu	Ala	Ser	Leu	Arg	Thr	Arg	Glu	Glu	Val	Ser	Arg	Thr	Arg	Val
225						230					235				240
Arg	Gly	Pro	Lys	Asp	Ser	Lys	Thr	Thr	Ala	Leu	Ile	Leu	Thr	Leu	Val
			245						250					255	
Val	Ala	Phe	Leu	Val	Cys	Trp	Ala	Pro	Tyr	His	Phe	Phe	Ala	Phe	Leu
			260					265					270		
Glu	Phe	Leu	Phe	Gln	Val	Gln	Ala	Val	Arg	Gly	Cys	Phe	Trp	Glu	Asp
			275				280					285			
Phe	Ile	Asp	Leu	Gly	Leu	Gln	Leu	Ala	Asn	Phe	Phe	Ala	Phe	Thr	Asn
			290			295					300				
Ser	Ser	Leu	Asn	Pro	Val	Ile	Tyr	Val	Phe	Val	Gly	Arg	Leu	Phe	Arg
305						310					315			320	
Thr	Lys	Val	Trp	Glu	Leu	Tyr	Lys	Gln	Cys	Thr	Pro	Lys	Ser	Leu	Ala
				325					330					335	
Pro	Ile	Ser	Ser	Ser	His	Arg	Lys	Glu	Ile	Phe	Gln	Leu	Phe	Trp	Arg

Asn

<210> 559
 <211> 1082
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (577)..(577)
 <223> wherein N is either a "C" or a "G".

<400> 559
 ctgtgcatgg catcatcctg gccccctcta gagctccaat cctccaacca gagccagctc 60
 ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120
 gtgctgccga catttatcat ctccatctgt ttcttcggcc tcctagggaa cctttttgtc 180
 ctgttggtct tcctctgccc cggcgaggaa ctgaacgtgg cagaaatcta cctggccaac 240
 ctggcagcct ctgatctggt gtttgtcttg ggcttgccct tctgggcaga gaatatctgg 300
 aaccagttta actggccttt cggagccctc ctctgccgtg tcatcaacgg ggtcatcaag 360
 gccaatttgt tcatcagcat cttcctgggtg gtggccatca gccaggaccg ctaccgcgtg 420
 ctgggtgcacc ctatggccag cgggaaggcag cagcggcgga ggcaggcccg ggtcacctgc 480
 gtgctcatct ggggttgtgg gggcctcttg agcatcccca cattcctgct gcgatccatc 540
 caagccgtcc cagatctgaa catcaccgcc tgcacgtgct tcctccccc tgaggcctgg 600
 cactttgcaa ggattgtgga gttaaatatt ctgggtttcc tcctaccact ggctgcgatc 660
 gtctttctta actaccacat cctggcctcc ctgcgaacgc gggaggagggt cagcaggaca 720
 agagtgcggg ggccgaagga tagcaagacc acagcgtgta tcctcacgct cgtggttgcc 780
 ttctgtgtct gctgggcccc ttaccacttc tttgccttcc tggaaattctt attccagggt 840
 caagcagtcc gaggtgctt ttggggaggac ttcatcgacc tgggcctgca attggccaac 900
 ttctttgctt tcaactaacag ctccctgaat ccagtaattt atgtctttgt gggccggctc 960
 ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgotccaata 1020
 tcttcatccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080
 cc 1082

<210> 560

<211> 353
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (191)..(191)
 <223> wherein Xaa is either "Leu" or "Val".

<400> 560

Met	Ala	Ser	Ser	Trp	Pro	Pro	Leu	Glu	Leu	Gln	Ser	Ser	Asn	Gln	Ser
1			5					10					15		
Gln	Leu	Phe	Pro	Gln	Asn	Ala	Thr	Ala	Cys	Asp	Asn	Ala	Pro	Glu	Ala
		20					25					30			
Trp	Asp	Leu	Leu	His	Arg	Val	Leu	Pro	Thr	Phe	Ile	Ile	Ser	Ile	Cys
		35					40				45				
Phe	Phe	Gly	Leu	Leu	Gly	Asn	Leu	Phe	Val	Leu	Leu	Val	Phe	Leu	Leu
	50				55					60					
Pro	Arg	Arg	Gln	Leu	Asn	Val	Ala	Glu	Ile	Tyr	Leu	Ala	Asn	Leu	Ala
65				70					75					80	
Ala	Ser	Asp	Leu	Val	Phe	Val	Leu	Gly	Leu	Pro	Phe	Trp	Ala	Glu	Asn
			85					90					95		
Ile	Trp	Asn	Gln	Phe	Asn	Trp	Pro	Phe	Gly	Ala	Leu	Leu	Cys	Arg	Val
		100					105						110		
Ile	Asn	Gly	Val	Ile	Lys	Ala	Asn	Leu	Phe	Ile	Ser	Ile	Phe	Leu	Val
		115				120					125				
Val	Ala	Ile	Ser	Gln	Asp	Arg	Tyr	Arg	Val	Leu	Val	His	Pro	Met	Ala
	130				135					140					
Ser	Gly	Arg	Gln	Gln	Arg	Arg	Gln	Ala	Arg	Val	Thr	Cys	Val	Leu	
145				150					155					160	
Ile	Trp	Val	Val	Gly	Gly	Leu	Leu	Ser	Ile	Pro	Thr	Phe	Leu	Leu	Arg
			165					170					175		
Ser	Ile	Gln	Ala	Val	Pro	Asp	Leu	Asn	Ile	Thr	Ala	Cys	Ile	Val	Leu
		180					185						190		
Leu	Pro	His	Glu	Ala	Trp	His	Phe	Ala	Arg	Ile	Val	Glu	Leu	Asn	Ile
		195					200					205			
Leu	Gly	Phe	Leu	Leu	Pro	Leu	Ala	Ala	Ile	Val	Phe	Phe	Asn	Tyr	His
	210				215						220				
Ile	Leu	Ala	Ser	Leu	Arg	Thr	Arg	Glu	Glu	Val	Ser	Arg	Thr	Arg	Val
225				230					235					240	

Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
245 250 255

Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
305 310 315 320

Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
325 330 335

Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
340 345 350

Asn

<210> 561
<211> 1082
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (705)..(705)
<223> wherein N is either a "G" or an "A".

<400> 561
ctgtgcatgg catcatcctg gccccctcta gagctccaat cctccaacca gagccagctc 60

ttccctcaaa atgctacggc ctgtgacaat gctccagaag cctgggacct gctgcacaga 120

gtgctgcaga catttatcat ctccatctgt ttcttcggcc tcctagggaa cctttttgtc 180

ctgttggtct tcctcctgcc ccggcggcaa ctgaacgtgg cagaaatcta cctggccaac 240

ctggcagcct ctgatctggt gtttgtcttg ggcttgcctt tctgggcaga gaatatctgg 300

aaccagtta actggccttt cggagccctc ctctgccgtg tcatcaacgg ggtcatcaag 360

gccaaattgt tcatcagcat ctctcctggt gtggccatca gccaggaccg ctaccgcgtg 420

ctggtgcacc ctatggccag cggaaggcag cagcggcgga ggcaggcccg ggtcacctgc 480

gtgctcatct ggggttgagg gggcctcttg agcatcccca cattcctgct gcgatccatc 540

caagccgtcc cagatctgaa catcaccgcc tgcatacctg tcctccccca tgaggcctgg 600

cactttgcaa ggatttgga gttaaatatt ctgggtttcc tcctaccact ggctgcgatc 660

gtcttcttca actaccacat cctggcctcc ctgcgaacgc gggaggagggt cagcaggaca 720
 agagtgcggg ggcgaagga tagcaagacc acagcgctga tcctcacgct cgtgggtgcc 780
 ttcttggtct gctgggcccc ttaccacttc tttgccttcc tggaattctt attccagggtg 840
 caagcagtcc gaggtgctt ttgggaggac ttcattgacc tgggcctgca attggccaac 900
 ttctttgctt tcactaacag ctccctgaat ccagtaattt atgtctttgt gggccggctc 960
 ttcaggacca aggtctggga actttataaa caatgcaccc ctaaaagtct tgctccaata 1020
 tttcatccc ataggaaaga aatcttccaa cttttctggc ggaattaaaa cagcattgaa 1080
 cc 1082

<210> 562
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 562

Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser
 1 5 10 15
 Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
 20 25 30
 Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys
 35 40 45
 Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Val Phe Leu Leu
 50 55 60
 Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
 65 70 75 80
 Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
 85 90 95
 Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
 100 105 110
 Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
 115 120 125
 Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
 130 135 140
 Ser Gly Arg Gln Gln Arg Arg Gln Ala Arg Val Thr Cys Val Leu
 145 150 155 160
 Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
 165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
 180 185 190
 Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
 195 200 205
 Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
 210 215 220
 Ile Leu Ala Ser Leu Arg Thr Arg Lys Glu Val Ser Arg Thr Arg Val
 225 230 235 240
 Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
 245 250 255
 Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
 260 265 270
 Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
 275 280 285
 Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
 290 295 300
 Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
 305 310 315 320
 Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
 325 330 335
 Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
 340 345 350

Asn

<210> 563
 <211> 3733
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (40)..(40)
 <223> wherein N is either a "C" or a "T".

 <400> 563
 atgttctctc cctggaagat atcaatgttt ctgtctgttt gtgaggactc cgtgccacc 60
 acggcctctt tcagcgccga catgctcaat gtcacctgc aagggccac tcttaacggg 120
 acctttgcc agagcaaatg cccccaagt gagtggtgg gctggctcaa caccatccag 180
 cccccccttc tctgggtgct gtctgtgctg gccaccctag agaacatctt tgtctctcagc 240

gtcttctgcc	tgacaaagag	cagctgcacg	gtggcagaga	tctacctggg	gaacctggcc	300
gcagcagacc	tgatcctggc	ctgggggctg	cccttctggg	ccatcaccat	ctccaacaac	360
ttcgactggc	tctttgggga	gacgctctgc	cgctgtggta	atgccattat	ctccatgaac	420
ctgtacagca	gcattctgtt	cctgatgctg	gtgagcatcg	accgtacct	ggccctgggtg	480
aaaaccatgt	ccatgggccc	gatgcggcgc	gtgcgctggg	ccaagctcta	cagcttggtg	540
atctgggggt	gtacgtgct	cctgagctca	cccattgctg	tgctccggac	catgaaggag	600
tacagcgatg	agggccacaa	cgtcaccgct	tgtgtcatca	gctacccatc	cctcatctgg	660
gaagtgttca	ccaacatgct	cctgaatgtc	gtgggcttcc	tgctgccctt	gagtgctatc	720
accttctgca	cgatgcagat	catgcagggtg	ctgcggaaca	acgagatgca	gaagttcaag	780
gagatccaga	cggagaggag	ggccacgggtg	ctagtctctg	ttgtgctgct	gctattcatc	840
atctgctggc	tgcccttcca	gatcagcacc	ttcctggata	cgctgcacgc	cctcggcatc	900
ctctccagct	gccaggacga	gcgcattcatc	gatgtaatca	cacagatcgc	ctccttcatg	960
gcctacagca	acagctgcct	caacccactg	gtgtacgtga	tcgtgggcaa	gcgcttccga	1020
aagaagtcct	gggagggtga	ccaggggagt	tgccagaaag	ggggctgcag	gtcagaaccc	1080
attcagatgg	agaactccat	gggcacactg	cggacctcca	tctccgtgga	acgcagatt	1140
cacaaactgc	aggactgggc	agggagcaga	cagtgcagaa	acgccagcag	ggctgctgtg	1200
aatttgtgta	aggattgagg	gacagttgct	tttcagcatg	ggcccaggaa	tgccaaggag	1260
acattctatgc	acgaccttgg	gaaattgagtt	gatgtctccg	gtaaaacacc	ggagactaat	1320
tcctgcctgt	cccaattttg	caggggagcat	ggctgtgagg	atgggggtga	ctcacgcaca	1380
gccaaaggact	ccaaaatcac	aacagcatta	ctgttcttat	ttgctgccac	acctgagcca	1440
gcctgctcct	tcccaggagt	ggaggaggcc	tggggggagg	gagaggagt	actgagcttc	1500
cctccctgtg	gtttctcgtc	cctgccccag	caagacaact	tagatctcca	ggagaactgc	1560
catccagcct	tggtgcaaat	gctgagtgca	caagtgagtt	gttgcctctg	gtttctttaa	1620
tctattcagc	tagaactttg	aaggacaatt	tcttgcatca	ataaagggtta	agccctgagg	1680
ggtccctgat	aacaacctgg	agaccaggat	tttatggctc	ccctcactga	tggacaagga	1740
ggtctgtgcc	aaagaagaat	ccaataagca	catattgagc	acttgctgta	tatgcagtat	1800
tgagcactgt	aggcaagacc	caagaaagag	aaggagccat	ctccattctt	aaggaaactca	1860
aagactcaag	tgggaacgac	tgggcactgc	caccaccaga	aagctgtctg	acgagacggt	1920
cgagcagggt	gctgtgggtg	atatggacag	cagaaggggg	agaccaaggt	tccagctcaa	1980

ccaataacta	ttgcacaacc	acctgtccct	gcttcagttc	ccttttatgt	aacatgaagt	2040
cgttgtgagg	gttaaaggca	gtaacagcta	taaagtaact	agaaaagcaa	aggggtgtac	2100
gtacatgtga	ggcatcatta	cgcagacgta	actgggatat	gtttactata	aggaaaagac	2160
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ccacctctgag	gccccaacgc	ccacacacac	aggagcattt	ggagagaagg	ccatgtcttc	2340
aaagtctgat	ttgtgatgag	gcagaggaag	atatttctaa	tcggtcttgc	ccagaggatc	2400
acagtgtcta	gaccccccac	caccagccgg	tacctgggaa	gggggagagt	gcaggcctgc	2460
tcaggggactg	ttctgtctc	agcaaccaag	ggattgttcc	tgtcaatcaa	tggtttatgtg	2520
gaagggtggc	cagtatgagc	cctagaagag	tgtgaaaagg	aatggcaatg	gtgttcacca	2580
tcggcagtg	cagggcagca	ctcattcact	tgataaatga	atatttatta	gctggttgga	2640
gagctagaac	ctggagagct	agaacctgga	gaactagaac	ctggagggct	agaacctgga	2700
gaggctagaa	ccaagaaggg	ctagaacctg	gaggggctag	aaccttagaga	agctaaaacc	2760
tgagctagaa	gctggaggac	tagaacctgg	agggctggaa	ctggaagggc	tagaacctgg	2820
agggctggaa	tctggagagc	tagaacctgg	agggctagaa	cctggagggc	tagaacctag	2880
aagggctaga	acctggaggg	ctggaatctg	gagagctaga	acctggaggg	ctagaacctg	2940
gagggctaga	acctagaagg	gctagaacct	ggagggctag	aacctggcag	gttagaacct	3000
agaagggcta	gaacctggag	agccagaacc	tggagggcta	gaacctggaa	gggctagaac	3060
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ctggagggaa	tgaacctgga	gggctagaac	ctggagaatg	agaaaaattt	acatggcaaa	3180
gagcccataa	atcctgacca	atccaactct	gaattttaaa	gcaaaagcgt	gaaaaaaaag	3240
attccctcct	tacccccaac	ccactctttt	ttcccaccac	ccactctcct	ctgcctcagt	3300
aagtatctgt	aggaagaaag	caggtgaaag	aagaagtaaa	aaccatttag	tattagtatt	3360
agaatgaagt	caaatctgtc	cacacatggt	gaatgaaaaa	aaaaaaaaag	aggctgtgtt	3420
ttgtcacaca	gggcagtcac	tcagcaccag	agcacgtgat	ggtctgagac	tctcttagga	3480
gcagagctct	gccgcaatgg	ccatgtgggg	atccacacct	ggtctgaggg	gcaactgagt	3540
ctgcgggaga	agagcggccc	tatgcatggt	gtagatgccc	tgataaagaa	catctgtcct	3600
gtgaaagact	caatgagctg	ttatgttgta	aacaggaagc	atttcacatc	caaacgagaa	3660

aatcatgtaa acatgtgtct tttctgtaga gcataataaa tggatgaggt ttttgcaaaa 3720

aaaaaaaaaa aaa 3733

<210> 564

<211> 391

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (14)..(14)

<223> wherein Xaa is either "Arg" or "Cys".

<400> 564

Met Phe Ser Pro Trp Lys Ile Ser Met Phe Leu Ser Val Cys Glu Asp
1 5 10 15

Ser Val Pro Thr Thr Ala Ser Phe Ser Ala Asp Met Leu Asn Val Thr
20 25 30

Leu Gln Gly Pro Thr Leu Asn Gly Thr Phe Ala Gln Ser Lys Cys Pro
35 40 45

Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu
50 55 60

Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser
65 70 75 80

Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu
85 90 95

Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe
100 105 110

Trp Ala Ile Thr Ile Ser Asn Asn Phe Asp Trp Leu Phe Gly Glu Thr
115 120 125

Leu Cys Arg Val Val Asn Ala Ile Ile Ser Met Asn Leu Tyr Ser Ser
130 135 140

Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu Val
145 150 155 160

Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu
165 170 175

Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro Met
180 185 190

Leu Val Phe Arg Thr Met Lys Glu Tyr Ser Asp Glu Gly His Asn Val
195 200 205

Thr Ala Cys Val Ile Ser Tyr Pro Ser Leu Ile Trp Glu Val Phe Thr
 210 215 220
 Asn Met Leu Leu Asn Val Val Gly Phe Leu Leu Pro Leu Ser Val Ile
 225 230 235 240
 Thr Phe Cys Thr Met Gln Ile Met Gln Val Leu Arg Asn Asn Glu Met
 245 250 255
 Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val
 260 265 270
 Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile
 275 280 285
 Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys
 290 295 300
 Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met
 305 310 315 320
 Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly
 325 330 335
 Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln
 340 345 350
 Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly
 355 360 365
 Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln
 370 375 380
 Asp Trp Ala Gly Ser Arg Gln
 385 390

<210> 565
 <211> 3733
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (933)..(933)
 <223> wherein N is either a "T" or a "C".
 <400> 565
 atgttctctc cctggaagat atcaatgttt ctgtctgttc gtgaggactc cgtgccacc 60
 acggcctctt tcagcgccga catgetcaat gtcacctgc aagggccac tcttaacggg 120
 acctttgcc agagcaaatg cccccaagtg gtagtgctgg gctggctcaa caccatccag 180
 ccccccttc tctgggtgct gttcgtgctg gccaccttag agaacatctt tgctctcagc 240
 gtctctgtgc tgcacaagag cagctgcacg gtggcagaga tctacctggg gaacctggcc 300

gcagcagacc	tgatcctggc	ctgcgggctg	cccttctggg	ccatcaccat	ctccaacaac	360
ttcgactggc	tctttgggga	gacgctctgc	cgcgtggtag	atgccattat	ctccatgaac	420
ctgtacagca	gcactctgtt	cctgatgctg	gtgagcatcg	accgctacct	ggccctgggt	480
aaaaccatgt	ccatggggcg	gatgcgcg	gtgcgctggg	ccaagctcta	cagcttggtg	540
atctgggggt	gtacgctgct	cctgagctca	cccatgctgg	tggtccggac	catgaaggag	600
tacagcgatg	agggccacaa	cgtcaccgct	tgtgtcatca	gctaccacat	cctcatctgg	660
gaagtgttca	ccaacatgct	cctgaatgtc	gtgggcttcc	tgctgccctc	gagtgtcatc	720
accttctgca	cgatgcagat	catgcagggt	ctgcggaaca	acgagatgca	gaagttcaag	780
gagatccaga	cggagaggag	ggccacgggt	ctagtctctg	ttgtgctgct	gctattcatc	840
atctgctggc	tgcccttcca	gatcagcacc	ttcctggata	cgtctgcatc	cctcggcatc	900
ctctccagct	gccaggacga	gcgcatcatc	gacgtaatca	cacagatcgc	ctccttcatg	960
gcctacagca	acagctgcct	caacccactg	gtgtacgtga	tcgtgggcaa	gcgcttccga	1020
aagaagtctt	gggagggtga	ccaggagggt	tgccagaaag	ggggctgcag	gtcagaacct	1080
attcagatgg	agaactccat	gggcacactg	cggacctcca	tctccgtgga	acgccagatt	1140
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tcctgccctg	cccaattttg	caggagcat	ggctgtgagg	atgggggtga	ctcacgcaca	1380
gccaggact	ccaaaatcac	aacagcatta	ctgttcttat	ttgctgccac	acctgagcca	1440
gcctgctcct	tcccaggagt	ggaggaggcc	tggggggagg	gagaggagtg	actgagcttc	1500
cctcccgctg	gttctccgtc	cctgcccag	caagacaact	tagatctcca	ggagaactgc	1560
catccagctt	tggtgcaatg	gctgagtgca	caagtgagtt	gttgccctgg	gtttcttttaa	1620
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aagactcaag	tgggaacgac	tgggcactgc	caccaccaga	aagctgttcg	acgagacggt	1920
cgagcagggt	gctgtgggtg	atatggacag	cagaaggggg	agaccaagggt	tccagctcaa	1980

ccaataacta	ttgcacaacc	acctgtccct	gcttcagttc	ccttttatgt	aacatgaagt	2040
cgttgtgagg	gttaaaggca	gtaacaggta	taaagtaact	agaaaagcaa	agggtgctac	2100
gtacatgtga	ggcatcatta	cgcagacgta	actgggatat	gtttactata	aggaaaagac	2160
actgagggtct	agaaatagct	ccgtggagca	gaatcagtat	tgggagccgg	tggcggtgtg	2220
aagcaccagt	gtctggcaca	cagtaggtgc	tcattggctc	ccttccacct	gtcattccca	2280
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acagtgtga	gacccccac	caccagccgg	tacctgggaa	gggggagagt	gcaggcctgc	2460
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gaagggtggc	cagtatgagc	cctagaagag	tgtgaaaagg	aatggcaatg	gtgttcacca	2580
tcggcagtgc	cagggcagca	ctcattcact	tgataaatga	atatattatta	gctggttgga	2640
gagctagaac	ctggagagct	agaacctgga	gaactagaac	ctggagggct	agaacctgga	2700
gaggctagaa	ccaagaagg	ctagaacctg	gaggggctag	aacctagaga	agctaaaacc	2760
tgagctagaa	gctggaggac	tagaacctgg	agggctggaa	tctgaagggc	tagaacctgg	2820
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gagggttaga	acctagaagg	gctagaacct	ggagggctag	aaactggcag	gttagaacct	3000
agaagggtcta	gaacctggag	agccagaacc	tggagggtcta	gaacctggaa	gggctagaac	3060
ctgtagagct	agaacatgga	gagctagaac	ccggcaggct	agaacctggc	aagctagaac	3120
ctggagggaa	tgaacctgga	gggctagaac	ctggagaatg	agaaaaattt	acatggcaaa	3180
gagcccataa	atcctgacca	atccaactct	gaattttaaa	gcaaaagcgt	gaaaaaaaag	3240
attccctcct	tacccccaac	ccactctttt	ttcccaccac	ccactctcct	ctgcctcagt	3300
aagtatctgg	aggaagaaaa	cagtgaaag	aagaagtaaa	aaccatttag	tattagtatt	3360
agaatgaagt	caaactgtgc	cacacatggt	gaatgaaaaa	aaaaaaaaag	aggctgtgtt	3420
ttgtcacaca	gggcagtcac	tcagcaccag	agcacgtgat	ggtctgagac	tctcttagga	3480
gcagagctct	gcccaatgg	ccatgtgggg	atccacacct	ggtctgaggg	gcaactgagt	3540
ctgcgggaga	agagcggccc	tatgcatggt	gtatagtcgc	tgataaagaa	catctgtcct	3600
gtgaaagact	caatgagctg	ttatgtttga	aacaggaagc	atttcacatc	caaacgagaa	3660
aatcatgtaa	acatgtgtct	tttctgtaga	gcataataaa	tggatgaggt	ttttgcaaaa	3720

aaaaaaaaaa aaa

3733

<210> 566
<211> 391
<212> PRT
<213> Homo sapiens

<400> 566

Met	Phe	Ser	Pro	Trp	Lys	Ile	Ser	Met	Phe	Leu	Ser	Val	Arg	Glu	Asp
1				5					10					15	
Ser	Val	Pro	Thr	Thr	Ala	Ser	Phe	Ser	Ala	Asp	Met	Leu	Asn	Val	Thr
			20					25					30		
Leu	Gln	Gly	Pro	Thr	Leu	Asn	Gly	Thr	Phe	Ala	Gln	Ser	Lys	Cys	Pro
		35					40					45			
Gln	Val	Glu	Trp	Leu	Gly	Trp	Leu	Asn	Thr	Ile	Gln	Pro	Pro	Phe	Leu
		50				55					60				
Trp	Val	Leu	Phe	Val	Leu	Ala	Thr	Leu	Glu	Asn	Ile	Phe	Val	Leu	Ser
65					70				75					80	
Val	Phe	Cys	Leu	His	Lys	Ser	Ser	Cys	Thr	Val	Ala	Glu	Ile	Tyr	Leu
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Gly	Asn	Leu	Ala	Ala	Ala	Asp	Leu	Ile	Leu	Ala	Cys	Gly	Leu	Pro	Phe
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Trp	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Phe	Asp	Trp	Leu	Phe	Gly	Glu	Thr
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Ile	Cys	Phe	Leu	Met	Leu	Val	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Leu	Val
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Lys	Thr	Met	Ser	Met	Gly	Arg	Met	Arg	Gly	Val	Arg	Trp	Ala	Lys	Leu
				165					170					175	
Tyr	Ser	Leu	Val	Ile	Trp	Gly	Cys	Thr	Leu	Leu	Leu	Ser	Ser	Pro	Met
			180					185						190	
Leu	Val	Phe	Arg	Thr	Met	Lys	Glu	Tyr	Ser	Asp	Glu	Gly	His	Asn	Val
			195				200					205			
Thr	Ala	Cys	Val	Ile	Ser	Tyr	Pro	Ser	Leu	Ile	Trp	Glu	Val	Phe	Thr
			210			215						220			
Asn	Met	Leu	Leu	Asn	Val	Val	Gly	Phe	Leu	Leu	Pro	Leu	Ser	Val	Ile
225					230						235				240
Thr	Phe	Cys	Thr	Met	Gln	Ile	Met	Gln	Val	Leu	Arg	Asn	Asn	Glu	Met

245 250 255
 Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val
 260 265 270
 Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile
 275 280 285
 Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys
 290 295 300
 Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met
 305 310 315 320
 Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly
 325 330 335
 Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln
 340 345 350
 Lys Gly Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly
 355 360 365
 Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln
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 Asp Trp Ala Gly Ser Arg Gln
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<210> 567
 <211> 3733
 <212> DNA
 <213> Homo sapiens

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 <222> (1061)..(1061)
 <223> wherein N is either a "G" or an "A".

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ccaataacta	ttgcacaacc	acctgtccct	gcctcagttc	ccttttatgt	aatatgaagt	2040
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<213> Homo sapiens

<220>

<221> VARIANT

<222> (354)..(354)

<223> wherein Xaa is either "Gly" or "Glu".

<400> 568

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		20						25					30		
Leu	Gln	Gly	Pro	Thr	Leu	Asn	Gly	Thr	Phe	Ala	Gln	Ser	Lys	Cys	Pro
	35						40				45				
Gln	Val	Glu	Trp	Leu	Gly	Trp	Leu	Asn	Thr	Ile	Gln	Pro	Pro	Phe	Leu
	50					55					60				
Trp	Val	Leu	Phe	Val	Leu	Ala	Thr	Leu	Glu	Asn	Ile	Phe	Val	Leu	Ser
	65				70					75				80	
Val	Phe	Cys	Leu	His	Lys	Ser	Ser	Cys	Thr	Val	Ala	Glu	Ile	Tyr	Leu
			85						90				95		
Gly	Asn	Leu	Ala	Ala	Ala	Asp	Leu	Ile	Leu	Ala	Cys	Gly	Leu	Pro	Phe
		100					105						110		
Trp	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Phe	Asp	Trp	Leu	Phe	Gly	Glu	Thr
		115					120					125			
Leu	Cys	Arg	Val	Val	Asn	Ala	Ile	Ile	Ser	Met	Asn	Leu	Tyr	Ser	Ser
	130				135						140				
Ile	Cys	Phe	Leu	Met	Leu	Val	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Leu	Val
	145				150					155				160	
Lys	Thr	Met	Ser	Met	Gly	Arg	Met	Arg	Gly	Val	Arg	Trp	Ala	Lys	Leu
			165						170					175	
Tyr	Ser	Leu	Val	Ile	Trp	Gly	Cys	Thr	Leu	Leu	Leu	Ser	Ser	Pro	Met
		180					185							190	
Leu	Val	Phe	Arg	Thr	Met	Lys	Glu	Tyr	Ser	Asp	Glu	Gly	His	Asn	Val
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Thr	Ala	Cys	Val	Ile	Ser	Tyr	Pro	Ser	Leu	Ile	Trp	Glu	Val	Phe	Thr
	210				215						220				
Asn	Met	Leu	Leu	Asn	Val	Val	Gly	Phe	Leu	Leu	Pro	Leu	Ser	Val	Ile
	225				230					235				240	
Thr	Phe	Cys	Thr	Met	Gln	Ile	Met	Gln	Val	Leu	Arg	Asn	Asn	Glu	Met
			245						250					255	

Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg Arg Ala Thr Val Leu Val
260 265 270

Leu Val Val Leu Leu Leu Phe Ile Ile Cys Trp Leu Pro Phe Gln Ile
275 280 285

Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys
290 295 300

Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met
305 310 315 320

Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly
325 330 335

Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln
340 345 350

Lys Glu Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly
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Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln
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Asp Trp Ala Gly Ser Arg Gln
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<210> 569

<211> 3405

<212> DNA

<213> Homo sapiens

<400> 569

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gctccttctc agccttggtg ctgtaactgc tgetcagtc accatgtagg aacaggccaa 180

gacatttttg gacaagtta accacgaagc cgaagacctg ttctatcaaa gtctacttgc 240

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agtgcctcta gaagacaaga gcaaacgggtt gaacacaatt ctaaatacaa tgagcaccat 480

ctacagtact ggaaaagttt gtaaccaga taatccaca gaatgcttat tacttgaacc 540

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aagctggaga tctgaggtcg gcaagcagct gaggccatta tatgaagagt atgtggtctt 660

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ggacgacttc ctgacagctc atcatgagat ggggcataac cagtatgata tggcatatgc	1260
tgcacaacct tttctgctaa gaaatggagc taatgaagga ttccatgaag ctgttgggga	1320
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 <211> 805
 <212> PRT
 <213> Homo sapiens

<400> 570

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 Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp
 35 40 45
 Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn
 50 55 60
 Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala
 65 70 75 80

Gln	Met	Tyr	Pro	Leu	Gln	Glu	Ile	Gln	Asn	Leu	Thr	Val	Lys	Leu	Gln	
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Leu	Gln	Ala	Leu	Gln	Gln	Asn	Gly	Ser	Ser	Val	Leu	Ser	Glu	Asp	Lys	
			100				105						110			
Ser	Lys	Arg	Leu	Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser	
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Thr	Gly	Lys	Val	Cys	Asn	Pro	Asp	Asn	Pro	Gln	Glu	Cys	Leu	Leu	Leu	
	130					135					140					
Glu	Pro	Gly	Leu	Asn	Glu	Ile	Met	Ala	Asn	Ser	Leu	Asp	Tyr	Asn	Glu	
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Arg	Leu	Trp	Ala	Trp	Glu	Ser	Trp	Arg	Ser	Glu	Val	Gly	Lys	Gln	Leu	
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Arg	Pro	Leu	Tyr	Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg	
		180						185					190			
Ala	Asn	His	Tyr	Glu	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu	
		195					200					205				
Val	Asn	Gly	Val	Asp	Gly	Tyr	Asp	Tyr	Ser	Arg	Gly	Gln	Leu	Ile	Glu	
	210					215					220					
Asp	Val	Glu	His	Thr	Phe	Glu	Glu	Ile	Lys	Pro	Leu	Tyr	Glu	His	Leu	
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His	Ala	Tyr	Val	Arg	Ala	Lys	Leu	Met	Asn	Ala	Tyr	Pro	Ser	Tyr	Ile	
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Ser	Pro	Ile	Gly	Cys	Leu	Pro	Ala	His	Leu	Leu	Gly	Asp	Met	Trp	Gly	
		260					265					270				
Arg	Phe	Trp	Thr	Asn	Leu	Tyr	Ser	Leu	Thr	Val	Pro	Phe	Gly	Gln	Lys	
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Pro	Asn	Ile	Asp	Val	Thr	Asp	Ala	Met	Val	Asp	Gln	Ala	Trp	Asp	Ala	
	290					295					300					
Gln	Arg	Ile	Phe	Lys	Glu	Ala	Glu	Lys	Phe	Phe	Val	Ser	Val	Gly	Leu	
	305				310					315					320	
Pro	Asn	Met	Thr	Gln	Gly	Phe	Trp	Glu	Asn	Ser	Met	Leu	Thr	Asp	Pro	
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Gly	Asn	Val	Gln	Lys	Ala	Val	Cys	His	Pro	Thr	Ala	Trp	Asp	Leu	Gly	
		340					345						350			
Lys	Gly	Asp	Phe	Arg	Ile	Leu	Met	Cys	Thr	Lys	Val	Thr	Met	Asp	Asp	
	355						360					365				
Phe	Leu	Thr	Ala	His	His	Glu	Met	Gly	His	Ile	Gln	Tyr	Asp	Met	Ala	
	370					375					380					

Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
 385 390 395 400
 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
 405 410 415
 His Leu Lys Ser Ile Gly Leu Leu Ser Pro Asp Phe Gln Glu Asp Asn
 420 425 430
 Glu Thr Glu Ile Asn Phe Leu Leu Lys Gln Ala Leu Thr Ile Val Gly
 435 440 445
 Thr Leu Pro Phe Thr Tyr Met Leu Glu Lys Trp Arg Trp Met Val Phe
 450 455 460
 Lys Gly Glu Ile Pro Lys Asp Gln Trp Met Lys Lys Trp Trp Glu Met
 465 470 475 480
 Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr
 485 490 495
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
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 Leu Cys Gln Ala Ala Lys His Glu Gly Pro Leu His Lys Cys Asp Ile
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 565 570 575
 Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe
 580 585 590
 Thr Trp Leu Lys Asp Gln Asn Lys Asn Ser Phe Val Gly Trp Ser Thr
 595 600 605
 Asp Trp Ser Pro Tyr Ala Asp Gln Ser Ile Lys Val Arg Ile Ser Leu
 610 615 620
 Lys Ser Ala Leu Gly Asp Lys Ala Tyr Glu Trp Asn Asp Asn Glu Met
 625 630 635 640
 Tyr Leu Phe Arg Ser Ser Val Ala Tyr Ala Met Arg Gln Tyr Phe Leu
 645 650 655
 Lys Val Lys Asn Gln Met Ile Leu Phe Gly Glu Glu Asp Val Arg Val
 660 665 670
 Ala Asn Leu Lys Pro Arg Ile Ser Phe Asn Phe Phe Val Thr Ala Pro
 675 680 685

Lys Asn Val Ser Asp Ile Ile Pro Arg Thr Glu Val Glu Lys Ala Ile
690 695 700

Arg Met Ser Arg Ser Arg Ile Asn Asp Ala Phe Arg Leu Asn Asp Asn
705 710 715 720

Ser Leu Glu Phe Leu Gly Ile Gln Pro Thr Leu Gly Pro Pro Asn Gln
725 730 735

Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val
740 745 750

Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg
755 760 765

Lys Lys Lys Asn Lys Ala Arg Ser Gly Glu Asn Pro Tyr Ala Ser Ile
770 775 780

Asp Ile Ser Lys Gly Glu Asn Asn Pro Gly Phe Gln Asn Thr Asp Asp
785 790 795 800

Val Gln Thr Ser Phe
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<210> 571
<211> 1284
<212> DNA
<213> Homo sapiens

<400> 571
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cagctgcacg ttgagcatga tgggtgagagt tgcagtaaca gctcccacca gcagattctg 120
gagacagggt agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccctc 180
cgcttctact acctgatcgc ttcgagagacc ccggggaaga acatcttttt ctecccgcgtg 240
agcatctcgg cggcctacgc catgctttcc ctgggggcct gctcacacag ccgcagccag 300
atccttgagg gcctgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc 360
ttccagcacc tctcgacac tctcaacctc cccggccatg ggctggaaac acgcgtgggc 420
agtgtcttgt tctgagcca caacctgaag ttcttgcaa aattcctgaa tgacaccatg 480
gccgtctatg aggcataaact ctteccaccc aactttctacg acactgtggg cacaatccag 540
cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggtcagtgag 600
ctcaagaagg acgtcttgat ggtgtgggtg aattacattt acttcaaagc cctgtggggg 660
aaaccattca tttctcaag gaccactccc aaagacttct atgttgatga gaacacaaca 720
gtccgggtgc ccatgatgct gcaggaccag gagcatcact ggtatcttca tgacagatac 780
ttgcctctgt cgggtgctacg gatggattac aaaggagacg caaccgtgtt ttctattctc 840

cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaattgagg 900
 tggaacaact tgttgccgaa gaggaatddd tacaagaagc tagagtgtca tcttcccaag 960
 ttctccattt ctggctccta tgtattagat cagattttgc ccaggctggg cttcacggat 1020
 ctgttctcca agtgggctga cttatccggc atcaccaaac agcaaaaact ggaggcatcc 1080
 aaaagtttcc acaaggccac cttggacgtg gatgaggctg gcaccgaggc tgcagcagcc 1140
 accacgttgc cgatcaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200
 cggcccttcc ttgtggtgat cttttccacc agcaccaga gtgtctcttt tctgggcaag 1260
 gtcgtcgacc ccacgaaacc atag 1284

<210> 572

<211> 427

<212> PRT

<213> Homo sapiens

<400> 572

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Val Gly Leu Leu Ala
 1 5 10 15
 Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser
 20 25 30
 Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser
 35 40 45
 Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr
 50 55 60
 Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu
 65 70 75 80
 Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His
 85 90 95
 Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu
 100 105 110
 Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu
 115 120 125
 Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe
 130 135 140
 Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met
 145 150 155 160
 Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val
 165 170 175

Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly
 180 185 190
 Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val
 195 200 205
 Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile
 210 215 220
 Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr
 225 230 235 240
 Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu
 245 250 255
 His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly
 260 265 270
 Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu
 275 280 285
 Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu
 290 295 300
 Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys
 305 310 315 320
 Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu
 325 330 335
 Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr
 340 345 350
 Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu
 355 360 365
 Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala
 370 375 380
 Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn
 385 390 395 400
 Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu
 405 410 415
 Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro
 420 425

<210> 573
 <211> 1284
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (699)..(699)

<223> wherein N is either a "C" or a "T".

<400> 573
 atgcacetta tgcactacct gctcctcctg ctggttgagc tactggccct ttctcatggc 60
 cagctgcacg ttgagcatga tgggtgagagt tgcagtaaca gctcccacca cgagattctg 120
 gagacaggtg aggggtcccc cagcctcaag atagccctcg ccaatgctga ctttgcttc 180
 cgcttctact acctgatcgc ttccggagacc ccggggaaga acatcttttt ctccccgctg 240
 agcatctcgg cggcctacgc catgctttcc ctgggggcct gctcacacag ccgcagccag 300
 atccttgagg gctggggtt caacctcacc gagctgtctg agtccgatgt ccataggggc 360
 ttccagcacc tctgcacac tctcaacctc cccggccatg ggtgggaac acgcgtgggc 420
 agtgctctgt tcttgagcca caacctgaag ttccttgcaa aattcctgaa tgacaccatg 480
 gccgtctatg aggctaaact ctccacacc aacttctacg acactgtggg cacaatccag 540
 cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggtcagtgag 600
 ctcaagaagg acgtcttgat ggtgctgggt aattacattt acttcaaagc cctgtgggag 660
 aaaccattca tttcctcaag gacctctccc aaagactttt atgttgatga gaacacaaca 720
 gtccgggtgc ccatgatgct gcaggaccag gagcatcact ggatcttca tgacagatac 780
 ttgcctctgt cggtgctacg gatggattac aaaggagacg caaccgtgtt ttctattctc 840
 cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaattagg 900
 tggaacaact tgttgcgga gaggaatttt tacaagaagc tagagtgtca tcttcccaag 960
 ttctccattt ctggctccta tgtattagat cagattttgc ccaggctggg cttcacggat 1020
 ctgtttccca agtgggctga cttatccggc atcaccaaac agcaaaaact ggaggcatcc 1080
 aaaagtttcc acaaggccac cttggacgtg gatgaggctg gcaccgagge tgcagcagcc 1140
 accacgttgc cgatcaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200
 cggcccttcc ttgtggtgat cttttccacc agcaccaga gtgtcctctt tctgggcaag 1260
 gtcgtcgacc ccacgaaacc atag 1284

<210> 574
 <211> 427
 <212> PRT
 <213> Homo sapiens

<400> 574

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Leu Val Gly Leu Leu Ala

1		5		10		15	
Leu	Ser	His	Gly	Gln	Leu	His	Val
		20				25	
Asn	Ser	Ser	His	Gln	Gln	Ile	Leu
		35				40	
Leu	Lys	Ile	Ala	Pro	Ala	Asn	Ala
	50				55		
Leu	Ile	Ala	Ser	Glu	Thr	Pro	Gly
	65			70			75
Ser	Ile	Ser	Ala	Ala	Tyr	Ala	Met
			85				90
Ser	Arg	Ser	Gln	Ile	Leu	Glu	Gly
			100			105	
Ser	Glu	Ser	Asp	Val	His	Arg	Gly
			115				120
Asn	Leu	Pro	Gly	His	Gly	Leu	Glu
		130				135	
Leu	Ser	His	Asn	Leu	Lys	Phe	Leu
	145			150			155
Ala	Val	Tyr	Glu	Ala	Lys	Leu	Phe
			165			170	
Gly	Thr	Ile	Gln	Leu	Ile	Asn	Asp
		180				185	
Lys	Ile	Val	Asp	Leu	Val	Ser	Glu
		195				200	
Leu	Val	Asn	Tyr	Ile	Tyr	Phe	Lys
	210			215			220
Ser	Ser	Arg	Thr	Thr	Pro	Lys	Asp
	225			230			235
Val	Arg	Val	Pro	Met	Met	Leu	Gln
			245			250	
His	Asp	Arg	Tyr	Leu	Pro	Cys	Ser
		260				265	
Asp	Ala	Thr	Val	Phe	Phe	Ile	Leu
		275				280	
Ile	Glu	Glu	Val	Leu	Thr	Pro	Glu
	290				295		300
Leu	Arg	Lys	Arg	Asn	Phe	Tyr	Lys

305 310 315 320
 Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu
 325 330 335
 Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr
 340 345 350
 Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu
 355 360 365
 Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala
 370 375 380
 Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn
 385 390 395 400
 Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu
 405 410 415
 Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro
 420 425

<210> 575

<211> 1284

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (597)..(597)

<223> wherein N is either a "T" or a "C".

<400> 575

atgcatctta tcgactacct gtccttcctg ctggttggac tactggccct ttctcatggc	60
cagctgcacg ttgagcatga tgggtgagagt tgcagtaaca gctcccacca gcagattctg	120
gagacaggtg agggctcccc cagcctcaag atagccctcg ccaatgctga ctttgccctc	180
cgtcttact acctgatcgc ttcggagacc ccggggaaga acatcttttt ctecccgctg	240
agcatctcgg cggcctacgc catgctttcc ctgggggcct gctcacacag ccgcagccag	300
atccttgagg gcctgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc	360
ttccagcacc tcttgacac tctcaacctc cccggccatg ggctggaaac acgcgtgggc	420
agtgtctgt tcttgagcca caacctgaag ttcttgcaa aattcctgaa tgacaccatg	480
gccgtctatg aggcataact cttccacacc aactctacg acactgtggg cacaatccag	540
cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggctcagcgag	600
ctcaagaagg acgtcttgat ggtgctggtg aattacattt acttcaaagc cctgtgggag	660

aaaccattca tttcctcaag gaccactccc aaagacttct atgttgatga gaacacaaca 720
 gtccgggtgc ccatgatgct gcaggaccag gagcatcaact ggatatctta tgacagatac 780
 ttgcctctgct cgggtgctacg gatggattac aaaggagacg caaccgtgtt tttcattctc 840
 cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaattgagg 900
 tggaacaact tgttgccgaa gaggaatttt tacaagaagc tagagttgca tcttcccaag 960
 ttctccattt ctggctccta tgtattagat cagattttgc ccaggctggg cttcacggat 1020
 ctgttctcca agtgggtgta cttatccggc atcaccaaac agcaaaaact ggaggcatcc 1080
 aaaagtttcc acaaggccac cttggacgtg gatgaggctg gcaccgaggc tgcagcagcc 1140
 accacgttgc cgatcaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200
 cggcccttcc ttgtggtgat cttttccacc agcaccacaga gtgtcctctt tctgggcaag 1260
 gtcgtcgacc ccacgaaacc atag 1284

<210> 576
 <211> 427
 <212> PRT
 <213> Homo sapiens
 <400> 576

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Val Gly Leu Leu Ala
 1 5 10 15
 Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser
 20 25 30
 Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser
 35 40 45
 Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr
 50 55 60
 Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu
 65 70 75 80
 Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His
 85 90 95
 Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu
 100 105 110
 Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu
 115 120 125
 Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe
 130 135 140

Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met
 145 150 155 160
 Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val
 165 170 175
 Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly
 180 185 190
 Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val
 195 200 205
 Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile
 210 215 220
 Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr
 225 230 235 240
 Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu
 245 250 255
 His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly
 260 265 270
 Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu
 275 280 285
 Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu
 290 295 300
 Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys
 305 310 315 320
 Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu
 325 330 335
 Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr
 340 345 350
 Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu
 355 360 365
 Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala
 370 375 380
 Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn
 385 390 395 400
 Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu
 405 410 415
 Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro
 420 425
 <210> 577
 <211> 1284
 <212> DNA

<213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (699)..(699)
 <223> wherein N is either a "C" or a "T".

<220>
 <221> misc_feature
 <222> (1143)..(1143)
 <223> wherein N is either a "C" or a "G".

<220>
 <221> misc_feature
 <222> (412)..(412)
 <223> wherein N is either a "C" or a "T".

<220>
 <221> misc_feature
 <222> (597)..(597)
 <223> wherein N is either a "T" or a "C".

<400> 577
 atgcacatcta tcgactacct gctcctcctg ctgggtggac tactggccct ttctcatggc 60
 cagctgcacg ttgagcatga tggtagagagt tgcagtaaca gctccacca gcagattctg 120
 gagacaggtg agggctcccc cagcctcaag atagccctg ccaatgctga ctttgccttc 180
 cgcttctact acctgatcgc ttccggagacc ccggggaaga acatcttttt ctccccgctg 240
 agcatctcgg cggcctacgc catgctttcc ctgggggcct gctcacacag ccgcagccag 300
 atccttgagg gcttgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc 360
 ttccagcacc tcctgcacac tctcaacctc ccgggccatg ggctggaaac angcgtgggc 420
 agtgctctgt tcctgagcca caacctgaag ttcttgcga aattctgaa tgacaccatg 480
 gccgtctatg aggtctaaact ctccacacc aacttctacg aactgtggg cacaatccag 540
 ctatcaaacg accacgtcaa gaaggaaact caggggaaga ttgtggattt ggtcagngag 600
 ctcaagaagg acgtcttgat ggtgctgggt aattacattt acttcaaaag cctgtggggag 660
 aaaccattca tttcctcaag gaccactccc aaagacttnt atgttgatga gaacacaaca 720
 gtccgggtgc ccatgatgct gcaggaccag gagcatcact ggtatcttca tgacagatac 780
 ttgccttctg cgggtgctacg gatggattac aaaggagacg caaccgtgtt ttctattctc 840
 cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaagtagg 900

tggaacaact tgttgcggaa gaggaatddd tacaagaagc tagagttgca tdtcccaag 960
 tdtccattt ctggctccta tgtattagat cagattttgc ccaggctggg dtccacggat 1020
 ctgttctcca agtgggctga cttatccggc atcaccaaac agcaaaaaat ggaggcatcc 1080
 aaaaagtttc acaaggccac ctggagctg gatgaggctg gcaccaggc tgcagcagcc 1140
 acnacgttcg cgtacaaatt cttctctgcc cagaccaatc gccacatcct gcgattcaac 1200
 cggcccttcc ttgtgtgat cttttccacc agcaccaga gtgtcctett tctgggcaag 1260
 gtcgtcgacc ccacgaaacc atag 1284

<210> 578
 <211> 427
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (138)..(138)
 <223> wherein Xaa is either "Arg" or a "Cys".

<400> 578

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Val Gly Leu Leu Ala
 1 5 10 15
 Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser
 20 25 30
 Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser
 35 40 45
 Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr
 50 55 60
 Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu
 65 70 75 80
 Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His
 85 90 95
 Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu
 100 105 110
 Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu
 115 120 125
 Asn Leu Pro Gly His Gly Leu Glu Thr Xaa Val Gly Ser Ala Leu Phe
 130 135 140
 Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met
 145 150 155 160

Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val
 165 170 175
 Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly
 180 185 190
 Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val
 195 200 205
 Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile
 210 215 220
 Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr
 225 230 235 240
 Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu
 245 250 255
 His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly
 260 265 270
 Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu
 275 280 285
 Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu
 290 295 300
 Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys
 305 310 315 320
 Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu
 325 330 335
 Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr
 340 345 350
 Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu
 355 360 365
 Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala
 370 375 380
 Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn
 385 390 395 400
 Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu
 405 410 415
 Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro
 420 425

<210> 579

<211> 18

<212> DNA

<213> Homo sapiens

<400> 579
tgtcatcaat ggggtcat 18

<210> 580
<211> 18
<212> DNA
<213> Homo sapiens

<400> 580
cggcggaggc aggcccg 18

<210> 581
<211> 18
<212> DNA
<213> Homo sapiens

<400> 581
gcctgcatcc tgctctc 18

<210> 582
<211> 18
<212> DNA
<213> Homo sapiens

<400> 582
acgcgggagg aggtcaga 18

<210> 583
<211> 18
<212> DNA
<213> Homo sapiens

<400> 583
tgagaaatgc gtgtattt 18

<210> 584
<211> 18
<212> DNA
<213> Homo sapiens

<400> 584
tgtctgttcg tgaggact 18

<210> 585
<211> 19
<212> DNA
<213> Homo sapiens

<400> 585
ccttccttcc gaagagaac 19

<210> 586
 <211> 19
 <212> DNA
 <213> Homo sapiens

<400> 586
 aaacacccgc acccaggaa

19

<210> 587
 <211> 19
 <212> DNA
 <213> Homo sapiens

<400> 587
 gtacgtggcg tacaagaa

19

<210> 588
 <211> 19
 <212> DNA
 <213> Homo sapiens

<400> 588
 atgacatcat taccagcc

19

<210> 589
 <211> 19
 <212> DNA
 <213> Homo sapiens

<400> 589
 catcatcgat gtaatcaca

19

<210> 590
 <211> 19
 <212> DNA
 <213> Homo sapiens

<400> 590
 gccagaaagg gggctgcag

19

<210> 591
 <211> 19
 <212> DNA
 <213> Homo sapiens

<400> 591
 caggagaact gccatccag

19

<210> 592
 <211> 19

<400> 598
attagtagcc tacctggt 18

<210> 599
<211> 19
<212> DNA
<213> Homo sapiens

<400> 599
gaatgctaata ataaagata 19

<210> 600
<211> 19
<212> DNA
<213> Homo sapiens

<400> 600
agaataatgc ttggcacac 19

<210> 601
<211> 19
<212> DNA
<213> Homo sapiens

<400> 601
atcagacaca tttttaggt 19

<210> 602
<211> 19
<212> DNA
<213> Homo sapiens

<400> 602
gcctgcagat gtcctgtac 19

<210> 603
<211> 19
<212> DNA
<213> Homo sapiens

<400> 603
caaagacttc tatgttgat 19

<210> 604
<211> 15
<212> DNA
<213> Homo sapiens

<400> 604
gagttagaac attag 15

<210>	605	
<211>	17	
<212>	DNA	
<213>	Homo sapiens	
<400>	605	
	cccacaaact gcttcgg	17
<210>	606	
<211>	21	
<212>	DNA	
<213>	Homo sapiens	
<400>	606	
	cttgagctca ctgaccaa c	21
<210>	607	
<211>	19	
<212>	DNA	
<213>	Homo sapiens	
<400>	607	
	gaggatggct atctcaga	19
<210>	608	
<211>	18	
<212>	DNA	
<213>	Homo sapiens	
<400>	608	
	tccacaacat ctgtggag	18
<210>	609	
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<212>	DNA	
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<400>	609	
	ccaaagttgt ggggatag	18
<210>	610	
<211>	19	
<212>	DNA	
<213>	Homo sapiens	
<400>	610	
	tgtttgtttg gttgtttg	19
<210>	611	
<211>	18	

<212>	DNA	
<213>	Homo sapiens	
<400>	611	
	tgatcatcaac ggggtcat	18
<210>	612	
<211>	18	
<212>	DNA	
<213>	Homo sapiens	
<400>	612	
	cggcggagac agggcccg	18
<210>	613	
<211>	18	
<212>	DNA	
<213>	Homo sapiens	
<400>	613	
	gcctgcatcg tgctctc	18
<210>	614	
<211>	18	
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 caacaaatta gtgggttga gg 22

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 <210> 768
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tgttaccccg tacagacaag g 21

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<210> 778
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<210> 779
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<210> 780
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<400> 780
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<210> 790
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<210> 792
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gcacacagga agaacacaca a 21

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<210> 795
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<210> 796
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<210> 797
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<400> 797
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<210> 798
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 <212> DNA
 <213> Homo sapiens

<400> 798
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<210> 799
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 <212> DNA
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<400> 799
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<210> 800
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<400> 800
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<210> 801
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<212> DNA
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<210> 802
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<400> 802
aaaaattagc tgggtgtggc t 21

<210> 803
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<210> 804
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<210> 805
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<400> 805
cactcttgtc ctgctgacct c 21

<210> 806
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ggttgtgctg ctgctattca t 21

<210> 809
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<213> Homo sapiens

<400> 809
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<210> 810
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<213> Homo sapiens

<400> 810
gccaccata aactgatctg a 21

<210> 811
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<213> Homo sapiens

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<210> 812
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<212> DNA
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<400> 812
gagctacgca aacatggaaa t 21

<210> 813
<211> 21
<212> DNA
<213> Homo sapiens

<400> 813
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<210> 814
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 <212> DNA
 <213> Homo sapiens

<400> 814
 gggttgctg ctgctattca t 21

<210> 815
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 <213> Homo sapiens

<400> 815
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<400> 816
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<210> 817
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<210> 818
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<400> 818
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<210> 819
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<400> 819
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<210> 820
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<212> DNA
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 <400> 820
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 <210> 821
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 <400> 821
 acatctggaa cccctcaaaa g 21

 <210> 822
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 <212> DNA
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 <400> 822
 tcttcagcaa aatttcatt gtt 23

 <210> 823
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 <212> DNA
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 <400> 823
 tcttcagcaa aatttcatt gtt 23

 <210> 824
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 cctcccccat gtctctctat c 21

 <210> 825
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 <400> 825
 cctcccccat gtctctctat c 21

 <210> 826
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 <213> Homo sapiens

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cacactgatt acctcttccg c 21

<210> 827
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<400> 827
cacactgatt acctcttccg c 21

<210> 828
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<400> 828
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<210> 829
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<400> 829
actttggatg cctccagttt t 21

<210> 830
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<213> Homo sapiens

<400> 830
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<210> 831
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<213> Homo sapiens

<400> 831
ccaacagagc aggaaatgaa g 21

<210> 832
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<400> 832
ccaacagagc aggaaatgaa g 21

<210> 833
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 833
 taagtgaacct gcccaaagtt g

21

<210> 834
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 834
 taagtgaacct gcccaaagtt g

21

<210> 835
 <211> 353
 <212> PRT
 <213> Mus musculus

<400> 835

Met Ala Ser Ser Trp Pro Pro Leu Glu Leu Gln Ser Ser Asn Gln Ser
 1 5 10 15

Gln Leu Phe Pro Gln Asn Ala Thr Ala Cys Asp Asn Ala Pro Glu Ala
 20 25 30

Trp Asp Leu Leu His Arg Val Leu Pro Thr Phe Ile Ile Ser Ile Cys
 35 40 45

Phe Phe Gly Leu Leu Gly Asn Leu Phe Val Leu Leu Val Phe Leu Leu
 50 55 60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
 65 70 75 80

Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
 85 90 95

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
 100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
 115 120 125

Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
 130 135 140

Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
 145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg

165 170 175
 Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
 180 185 190
 Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
 195 200 205
 Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
 210 215 220
 Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
 225 230 235 240
 Arg Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
 245 250 255
 Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
 260 265 270
 Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
 275 280 285
 Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
 290 295 300
 Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
 305 310 315 320
 Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
 325 330 335
 Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
 340 345 350
 Asn

<210> 836
 <211> 352
 <212> PRT
 <213> *Oryctolagus cuniculus*

<400> 836

Met Ala Ser Gln Gly Pro Leu Glu Leu Gln Pro Ser Asn Gln Ser Gln
 1 5 10 15
 Leu Ala Pro Pro Asn Ala Thr Ser Cys Ser Gly Ala Pro Asp Ala Trp
 20 25 30
 Asp Leu Leu His Arg Leu Leu Pro Thr Phe Ile Ile Ala Ile Phe Thr
 35 40 45
 Leu Gly Leu Leu Gly Asn Ser Phe Val Leu Ser Val Phe Leu Leu Ala
 50 55 60

Arg Arg Arg Leu Ser Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala Ala
 65 70 75 80
 Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn Val
 85 90 95
 Arg Asn Gln Phe Asp Trp Pro Phe Gly Ala Ala Leu Cys Arg Ile Val
 100 105 110
 Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val Val
 115 120 125
 Ala Ile Ser Gln Asp Arg Tyr Ser Val Leu Val His Pro Met Ala Ser
 130 135 140
 Arg Arg Gly Arg Arg Arg Arg Gln Ala Gln Ala Thr Cys Ala Leu Ile
 145 150 155 160
 Trp Leu Ala Gly Gly Leu Leu Ser Thr Pro Thr Phe Val Leu Arg Ser
 165 170 175
 Val Arg Ala Val Pro Glu Leu Asn Val Ser Ala Cys Ile Leu Leu Leu
 180 185 190
 Pro His Glu Ala Trp His Trp Leu Arg Met Val Glu Leu Asn Leu Leu
 195 200 205
 Gly Phe Leu Leu Pro Leu Ala Ala Ile Leu Phe Phe Asn Cys His Ile
 210 215 220
 Leu Ala Ser Leu Arg Arg Arg Gly Glu Arg Val Pro Ser Arg Cys Gly
 225 230 235 240
 Gly Pro Arg Asp Ser Lys Ser Thr Ala Leu Ile Leu Thr Leu Val Ala
 245 250 255
 Ser Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu Glu
 260 265 270
 Cys Leu Trp Gln Val His Ala Ile Gly Gly Cys Phe Trp Glu Glu Phe
 275 280 285
 Thr Asp Leu Gly Leu Gln Leu Ser Asn Phe Ser Ala Phe Val Asn Ser
 290 295 300
 Cys Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg Thr
 305 310 315 320
 Lys Val Trp Glu Leu Cys Gln Gln Cys Ser Pro Arg Ser Leu Ala Pro
 325 330 335
 Val Ser Ser Ser Arg Arg Lys Glu Met Leu Trp Gly Phe Trp Arg Asn
 340 345 350
 <210> 837
 <211> 337
 <212> PRT

<213> Rattus norvegicus

<400> 837

Met Ala Ser Glu Val Leu Leu Glu Leu Gln Pro Ser Asn Arg Ser Leu
1 5 10 15
Gln Ala Pro Ala Asn Ile Thr Ser Cys Glu Ser Ala Leu Glu Asp Trp
20 25 30
Asp Leu Leu Tyr Arg Val Leu Pro Gly Phe Val Ile Thr Ile Cys Phe
35 40 45
Phe Gly Leu Leu Gly Asn Leu Leu Val Leu Ser Phe Phe Leu Leu Pro
50 55 60
Trp Arg Gln Trp Trp Trp Gln Gln Arg Gln Arg Gln Gln Arg Leu Thr
65 70 75 80
Ile Ala Glu Ile Tyr Leu Ala Asn Leu Ala Ala Ser Asp Leu Val Phe
85 90 95
Val Leu Gly Leu Pro Phe Trp Ala Glu Asn Ile Gly Asn Arg Phe Asn
100 105 110
Trp Pro Phe Gly Thr Asp Leu Cys Arg Val Val Ser Gly Val Ile Lys
115 120 125
Ala Asn Leu Phe Val Ser Ile Phe Leu Val Val Ala Ile Ser Gln Asp
130 135 140
Arg Tyr Arg Leu Leu Val Tyr Pro Met Thr Ser Trp Gly Tyr Arg Arg
145 150 155 160
Arg Arg Gln Ala Gln Ala Thr Cys Leu Leu Ile Trp Val Ala Gly Gly
165 170 175
Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg Ser Val Lys Val Val Pro
180 185 190
Asp Leu Asn Val Ser Ala Cys Ile Leu Leu Phe Pro His Glu Ala Trp
195 200 205
His Phe Ala Arg Met Val Glu Leu Asn Val Leu Gly Phe Leu Leu Pro
210 215 220
Val Thr Ala Ile Ile Phe Phe Asn Tyr His Ile Leu Ala Ser Leu Arg
225 230 235 240
Gly Gln Lys Glu Ala Ser Arg Thr Arg Cys Gly Gly Pro Lys Gly Ser
245 250 255
Lys Thr Thr Gly Leu Ile Leu Thr Leu Val Ala Ser Phe Leu Val Cys
260 265 270
Trp Cys Pro Tyr His Phe Phe Ala Phe Leu Asp Phe Leu Val Gln Val
275 280 285

Arg Val Ile Gln Asp Cys Ser Trp Lys Glu Ile Thr Asp Leu Gly Leu
290 295 300

Gln Leu Ala Asn Phe Phe Ala Phe Val Asn Ser Cys Leu Asn Pro Leu
305 310 315 320

Ile Tyr Val Phe Ala Gly Arg Leu Leu Lys Thr Arg Val Leu Gly Thr
325 330 335

Leu

<210> 838

<211> 392

<212> PRT

<213> Mus musculus

<400> 838

Met Pro Cys Ser Trp Lys Leu Leu Gly Phe Leu Ser Val His Glu Pro
1 5 10 15

Met Pro Thr Ala Ala Ser Phe Gly Ile Glu Met Phe Asn Val Thr Thr
20 25 30

Gln Val Leu Gly Ser Ala Leu Asn Gly Thr Leu Ser Lys Asp Asn Cys
35 40 45

Pro Asp Thr Glu Trp Trp Ser Trp Leu Asn Ala Ile Gln Ala Pro Phe
50 55 60

Leu Trp Val Leu Phe Leu Leu Ala Ala Leu Glu Asn Leu Phe Val Leu
65 70 75 80

Ser Val Phe Phe Leu His Lys Asn Ser Cys Thr Val Ala Glu Ile Tyr
85 90 95

Leu Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro
100 105 110

Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp Trp Val Phe Gly Glu
115 120 125

Val Leu Cys Arg Val Val Asn Thr Met Ile Tyr Met Asn Leu Tyr Ser
130 135 140

Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg Tyr Leu Ala Leu
145 150 155 160

Val Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys
165 170 175

Leu Tyr Ser Leu Val Ile Trp Gly Cys Thr Leu Leu Leu Ser Ser Pro
180 185 190

Met Leu Val Phe Arg Thr Met Arg Glu Tyr Ser Glu Glu Gly His Asn

195 200 205
 Val Thr Ala Cys Val Ile Val Tyr Pro Ser Arg Ser Trp Glu Val Phe
 210 215 220
 Thr Asn Val Leu Leu Asn Leu Val Gly Phe Leu Leu Pro Leu Ser Val
 225 230 235 240
 Ile Thr Phe Cys Thr Val Arg Ile Leu Gln Val Leu Arg Asn Asn Glu
 245 250 255
 Met Lys Lys Phe Lys Glu Val Gln Thr Glu Arg Lys Ala Thr Val Leu
 260 265 270
 Val Leu Ala Val Leu Gly Leu Phe Val Leu Cys Trp Val Pro Phe Gln
 275 280 285
 Ile Ser Thr Phe Leu Asp Thr Leu Leu Arg Leu Gly Val Leu Ser Gly
 290 295 300
 Cys Trp Asp Glu His Ala Val Asp Val Ile Thr Gln Ile Ser Ser Tyr
 305 310 315 320
 Val Ala Tyr Ser Asn Ser Gly Leu Asn Pro Leu Val Tyr Val Ile Val
 325 330 335
 Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu Val Tyr Arg Val Leu Cys
 340 345 350
 Gln Lys Gly Gly Cys Met Gly Glu Pro Val Gln Met Glu Asn Ser Met
 355 360 365
 Gly Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu
 370 375 380
 Gln Asp Trp Ala Gly Lys Lys Gln
 385 390

<210> 839
 <211> 367
 <212> PRT
 <213> *Oryctolagus cuniculus*

<400> 839

Met Leu Asn Ile Thr Ser Gln Val Leu Ala Pro Ala Leu Asn Gly Ser
 1 5 10 15
 Val Ser Gln Ser Ser Gly Cys Pro Asn Thr Glu Trp Ser Gly Trp Leu
 20 25 30
 Asn Val Ile Gln Ala Pro Phe Leu Trp Val Leu Phe Val Leu Ala Thr
 35 40 45
 Leu Glu Asn Leu Phe Val Leu Ser Val Phe Cys Leu His Lys Ser Ser
 50 55 60

Cys Thr Val Ala Glu Val Tyr Leu Gly Asn Leu Ala Ala Ala Asp Leu
 65 70 75 80
 Ile Leu Ala Cys Gly Leu Pro Phe Trp Ala Val Thr Ile Ala Asn His
 85 90 95
 Phe Asp Trp Leu Phe Gly Glu Ala Leu Cys Arg Val Val Asn Thr Met
 100 105 110
 Ile Tyr Met Asn Leu Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser
 115 120 125
 Ile Asp Arg Tyr Leu Ala Leu Val Lys Thr Met Ser Ile Gly Arg Met
 130 135 140
 Arg Arg Val Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Gly Cys
 145 150 155 160
 Thr Leu Leu Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp
 165 170 175
 Tyr Arg Asp Glu Gly Tyr Asn Val Thr Ala Cys Ile Ile Asp Tyr Pro
 180 185 190
 Ser Arg Ser Trp Glu Val Phe Thr Asn Val Leu Leu Asn Leu Val Gly
 195 200 205
 Phe Leu Leu Pro Leu Ser Val Ile Thr Phe Cys Thr Val Gln Ile Leu
 210 215 220
 Gln Val Leu Arg Asn Asn Glu Met Gln Lys Phe Lys Glu Ile Gln Thr
 225 230 235 240
 Glu Arg Arg Ala Thr Val Leu Val Leu Ala Val Leu Leu Leu Phe Val
 245 250 255
 Val Cys Trp Leu Pro Phe Gln Val Ser Thr Phe Leu Asp Thr Leu Leu
 260 265 270
 Lys Leu Gly Val Leu Ser Ser Cys Trp Asp Glu His Val Ile Asp Val
 275 280 285
 Ile Thr Gln Val Gly Ser Phe Met Gly Tyr Ser Asn Ser Cys Leu Asn
 290 295 300
 Pro Leu Val Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg
 305 310 315 320
 Glu Val Tyr Arg Ala Ala Cys Pro Lys Ala Gly Cys Val Leu Glu Pro
 325 330 335
 Val Gln Ala Glu Ser Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val
 340 345 350
 Glu Arg Gln Ile His Lys Leu Pro Glu Trp Thr Arg Ser Ser Gln
 355 360 365

<210> 840
 <211> 372
 <212> PRT
 <213> Cavia porcellus

<400> 840

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Met Phe Asn Ile Thr Ser Gln Val Ser Ala Leu Asn Ala Thr Leu Ala
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Gln Gly Asn Ser Cys Leu Asp Ala Glu Trp Trp Ser Trp Leu Asn Thr
          20          25          30

Ile Gln Ala Pro Phe Leu Trp Val Leu Phe Val Leu Ala Val Leu Glu
          35          40          45

Asn Ile Phe Val Leu Ser Val Phe Phe Leu His Lys Ser Ser Cys Thr
50          55          60

Val Ala Glu Ile Tyr Leu Gly Asn Leu Ala Val Ala Asp Leu Ile Leu
65          70          75          80

Ala Phe Gly Leu Pro Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp
          85          90          95

Trp Leu Phe Gly Glu Val Leu Cys Arg Met Val Asn Thr Met Ile Gln
100          105          110

Met Asn Met Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp
115          120          125

Arg Tyr Leu Ala Leu Val Lys Thr Met Ser Met Gly Arg Met Arg Gly
130          135          140

Val Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Gly Cys Ala Leu
145          150          155          160

Leu Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp Tyr Arg
          165          170          175

Asp Glu Gly His Asn Val Thr Ala Cys Leu Ile Ile Tyr Pro Ser Leu
180          185          190

Thr Trp Gln Val Phe Thr Asn Val Leu Leu Asn Leu Val Gly Phe Leu
195          200          205

Leu Pro Leu Ser Ile Ile Thr Phe Cys Thr Val Gln Ile Met Gln Val
210          215          220

Leu Arg Asn Asn Glu Met Gln Lys Phe Lys Glu Ile Gln Thr Glu Arg
225          230          235          240

Arg Ala Thr Val Leu Val Leu Ala Val Leu Leu Phe Val Val Cys
245          250          255

Trp Leu Pro Phe Gln Ile Gly Thr Phe Leu Asp Thr Leu Arg Leu Leu
260          265          270

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Gly Phe Leu Pro Gly Cys Trp Glu His Val Ile Asp Leu Ile Thr Gln
275 280 285

Ile Ser Ser Tyr Leu Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val
290 295 300

Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu Val Tyr
305 310 315 320

His Gly Leu Cys Arg Ser Gly Gly Cys Val Ser Glu Pro Ala Gln Ser
325 330 335

Glu Asn Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val Asp Arg Gln
340 345 350

Ile His Lys Leu Gln Asp Trp Ala Arg Ser Ser Ser Glu Gly Thr Pro
355 360 365

Pro Gly Leu Leu
370

<210> 841

<211> 396

<212> PRT

<213> Rattus norvegicus

<400> 841

Met Asp Thr Arg Ser Ser Leu Cys Pro Lys Thr Gln Ala Val Val Ala
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Val Phe Trp Gly Pro Gly Cys His Leu Ser Thr Cys Ile Glu Met Phe
20 25 30

Asn Ile Thr Thr Gln Ala Leu Gly Ser Ala His Asn Gly Thr Phe Ser
35 40 45

Glu Val Asn Cys Pro Asp Thr Glu Trp Trp Ser Trp Leu Asn Ala Ile
50 55 60

Gln Ala Pro Phe Leu Trp Val Leu Phe Leu Leu Ala Ala Leu Glu Asn
65 70 75 80

Ile Phe Val Leu Ser Val Phe Cys Leu His Lys Thr Asn Cys Thr Val
85 90 95

Ala Glu Ile Tyr Leu Gly Asn Leu Ala Ala Asp Leu Ile Leu Ala
100 105 110

Cys Gly Leu Pro Phe Trp Ala Ile Thr Ile Ala Asn Asn Phe Asp Trp
115 120 125

Leu Phe Gly Glu Val Leu Cys Arg Val Val Asn Thr Met Ile Tyr Met
130 135 140

Asn Leu Tyr Ser Ser Ile Cys Phe Leu Met Leu Val Ser Ile Asp Arg

145 150 155 160
 Tyr Leu Ala Leu Val Lys Thr Met Ser Met Gly Arg Met Arg Gly Val
 165 170 175
 Arg Trp Ala Lys Leu Tyr Ser Leu Val Ile Trp Ser Cys Thr Leu Leu
 180 185 190
 Leu Ser Ser Pro Met Leu Val Phe Arg Thr Met Lys Asp Tyr Arg Glu
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 Glu Gly His Asn Val Thr Ala Cys Val Ile Val Tyr Pro Ser Arg Ser
 210 215 220
 Trp Glu Val Phe Thr Asn Met Leu Leu Asn Leu Val Gly Phe Leu Leu
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 Pro Leu Ser Ile Ile Thr Phe Cys Thr Val Arg Ile Met Gln Val Leu
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 Arg Asn Asn Glu Met Lys Lys Phe Lys Glu Val Gln Thr Glu Lys Lys
 260 265 270
 Ala Thr Val Leu Val Leu Ala Val Leu Gly Leu Phe Val Leu Cys Trp
 275 280 285
 Phe Pro Phe Gln Ile Ser Thr Phe Leu Asp Thr Leu Leu Arg Leu Gly
 290 295 300
 Val Leu Ser Gly Cys Trp Asn Glu Arg Ala Val Asp Ile Val Thr Gln
 305 310 315 320
 Ile Ser Ser Tyr Val Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val
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 Tyr Val Ile Val Gly Lys Arg Phe Arg Lys Lys Ser Arg Glu Val Tyr
 340 345 350
 Gln Ala Ile Cys Arg Lys Gly Gly Cys Met Gly Glu Ser Val Gln Met
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 Glu Asn Ser Met Gly Thr Leu Arg Thr Ser Ile Ser Val Asp Arg Gln
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 Ile His Lys Leu Gln Asp Trp Ala Gly Asn Lys Gln
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 <210> 842
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 <212> DNA
 <213> homo sapiens

 <220>
 <221> misc_feature
 <222> (2173)..(2173)
 <223> wherein N is either a "T" or a "C".

[illegible]

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3405

<210> 843
<211> 805
<212> PRT
<213> homo sapiens

<400> 843

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			20					25					30		
Asn	His	Glu	Ala	Glu	Asp	Leu	Phe	Tyr	Gln	Ser	Ser	Leu	Ala	Ser	Trp
		35					40					45			
Asn	Tyr	Asn	Thr	Asn	Ile	Thr	Glu	Glu	Asn	Val	Gln	Asn	Met	Asn	Asn
		50				55					60				
Ala	Gly	Asp	Lys	Trp	Ser	Ala	Phe	Leu	Lys	Glu	Gln	Ser	Thr	Leu	Ala
	65					70				75					80
Gln	Met	Tyr	Pro	Leu	Gln	Glu	Ile	Gln	Asn	Leu	Thr	Val	Lys	Leu	Gln
				85					90					95	
Leu	Gln	Ala	Leu	Gln	Gln	Asn	Gly	Ser	Ser	Val	Leu	Ser	Glu	Asp	Lys
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Ser	Lys	Arg	Leu	Asn	Thr	Ile	Leu	Asn	Thr	Met	Ser	Thr	Ile	Tyr	Ser
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Arg	Leu	Trp	Ala	Trp	Glu	Ser	Trp	Arg	Ser	Glu	Val	Gly	Lys	Gln	Leu
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Arg	Pro	Leu	Tyr	Glu	Glu	Tyr	Val	Val	Leu	Lys	Asn	Glu	Met	Ala	Arg
			180					185					190		
Ala	Asn	His	Tyr	Glu	Asp	Tyr	Gly	Asp	Tyr	Trp	Arg	Gly	Asp	Tyr	Glu
		195					200						205		
Val	Asn	Gly	Val	Asp	Gly	Tyr	Asp	Tyr	Ser	Arg	Gly	Gln	Leu	Ile	Glu
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 Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala
 290 295 300
 Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
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 Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro
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 Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly
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 Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp
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 Phe Leu Thr Ala His His Glu Met Gly His Ile Gln Tyr Asp Met Ala
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 Tyr Ala Ala Gln Pro Phe Leu Leu Arg Asn Gly Ala Asn Glu Gly Phe
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 His Glu Ala Val Gly Glu Ile Met Ser Leu Ser Ala Ala Thr Pro Lys
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 Lys Arg Glu Ile Val Gly Val Val Glu Pro Val Pro His Asp Glu Thr
 485 490 495
 Tyr Cys Asp Pro Ala Ser Leu Phe His Val Ser Asn Asp Tyr Ser Phe
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 Ile Arg Tyr Tyr Thr Arg Thr Leu Tyr Gln Phe Gln Phe Gln Glu Ala
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Gly Lys Ser Glu Pro Trp Thr Leu Ala Leu Glu Asn Val Val Gly Ala
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 Lys Asn Met Asn Val Arg Pro Leu Leu Asn Tyr Phe Glu Pro Leu Phe
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 Pro Pro Val Ser Ile Trp Leu Ile Val Phe Gly Val Val Met Gly Val
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 Ile Val Val Gly Ile Val Ile Leu Ile Phe Thr Gly Ile Arg Asp Arg
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<210> 844
 <211> 3733
 <212> DNA
 <213> homo sapiens

<220>
 <221> misc_feature
 <222> (40)..(40)

<223> wherein N is either a "C" or a "T".

<220>

<221> misc_feature

<222> (47)..(47)

<223> wherein N is either an "A" or a "C".

<220>

<221> misc_feature

<222> (933)..(933)

<223> wherein N is either a "T" or a "C".

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<221> misc_feature

<222> (1061)..(1061)

<223> wherein N is either a "G" or an "A".

<400> 844

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<210> 845
<211> 391
<212> PRT
<213> homo sapiens

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<220>
<221> VARIANT
<222> (14)..(14)
<223> wherein Xaa is either "Arg" or a "Cys".

```

```

<220>
<221> VARIANT
<222> (16)..(16)
<223> wherein Xaa is either "Asp" or a "Ala".

```

```

<220>
<221> VARIANT
<222> (354)..(354)
<223> wherein Xaa is either "Gly" or a "Glu".

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<400> 845

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			20					25					30		
Leu	Gln	Gly	Pro	Thr	Leu	Asn	Gly	Thr	Phe	Ala	Gln	Ser	Lys	Cys	Pro
		35					40					45			
Gln	Val	Glu	Trp	Leu	Gly	Trp	Leu	Asn	Thr	Ile	Gln	Pro	Pro	Phe	Leu
		50				55					60				
Trp	Val	Leu	Phe	Val	Leu	Ala	Thr	Leu	Glu	Asn	Ile	Phe	Val	Leu	Ser
65					70					75					80
Val	Phe	Cys	Leu	His	Lys	Ser	Ser	Cys	Thr	Val	Ala	Glu	Ile	Tyr	Leu
				85					90					95	
Gly	Asn	Leu	Ala	Ala	Ala	Asp	Leu	Ile	Leu	Ala	Cys	Gly	Leu	Pro	Phe
			100					105					110		
Trp	Ala	Ile	Thr	Ile	Ser	Asn	Asn	Phe	Asp	Trp	Leu	Phe	Gly	Glu	Thr
			115				120						125		
Leu	Cys	Arg	Val	Val	Asn	Ala	Ile	Ile	Ser	Met	Asn	Leu	Tyr	Ser	Ser
		130				135					140				
Ile	Cys	Phe	Leu	Met	Leu	Val	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Leu	Val
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Lys	Thr	Met	Ser	Met	Gly	Arg	Met	Arg	Gly	Val	Arg	Trp	Ala	Lys	Leu
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Tyr	Ser	Leu	Val	Ile	Trp	Gly	Cys	Thr	Leu	Leu	Leu	Ser	Ser	Pro	Met
			180					185						190	
Leu	Val	Phe	Arg	Thr	Met	Lys	Glu	Tyr	Ser	Asp	Glu	Gly	His	Asn	Val
			195				200					205			
Thr	Ala	Cys	Val	Ile	Ser	Tyr	Pro	Ser	Leu	Ile	Trp	Glu	Val	Phe	Thr
			210			215					220				
Asn	Met	Leu	Leu	Asn	Val	Val	Gly	Phe	Leu	Leu	Pro	Leu	Ser	Val	Ile
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Thr	Phe	Cys	Thr	Met	Gln	Ile	Met	Gln	Val	Leu	Arg	Asn	Asn	Glu	Met
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Gln	Lys	Phe	Lys	Glu	Ile	Gln	Thr	Glu	Arg	Arg	Ala	Thr	Val	Leu	Val
			260					265					270		
Leu	Val	Val	Leu	Leu	Leu	Phe	Ile	Ile	Cys	Trp	Leu	Pro	Phe	Gln	Ile
			275				280						285		

Ser Thr Phe Leu Asp Thr Leu His Arg Leu Gly Ile Leu Ser Ser Cys
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Gln Asp Glu Arg Ile Ile Asp Val Ile Thr Gln Ile Ala Ser Phe Met
 305 310 315 320

Ala Tyr Ser Asn Ser Cys Leu Asn Pro Leu Val Tyr Val Ile Val Gly
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Lys Arg Phe Arg Lys Lys Ser Trp Glu Val Tyr Gln Gly Val Cys Gln
 340 345 350

Lys Xaa Gly Cys Arg Ser Glu Pro Ile Gln Met Glu Asn Ser Met Gly
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Thr Leu Arg Thr Ser Ile Ser Val Glu Arg Gln Ile His Lys Leu Gln
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Asp Trp Ala Gly Ser Arg Gln
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<210> 846
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<400> 846
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<400> 847

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Asn Thr Thr Met Ser Leu Thr Ala Leu Arg Gln Gln Met Gln Thr Gln
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Asn Leu Ser Ala Tyr Ile Ile Pro Gly Thr Asp Ala His Met Asn Glu
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Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr
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Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp
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Thr Asp Ser Arg Tyr Trp Thr Gln Ala Glu Arg Gln Met Asp Cys Asn
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 Leu Thr Glu Ile Pro Ala Gly Gly Arg Val Gly Phe Asp Pro Phe Leu
 145 150 155 160
 Leu Ser Ile Asp Thr Trp Glu Ser Tyr Asp Leu Ala Leu Gln Gly Ser
 165 170 175
 Asn Arg Gln Leu Val Ser Ile Thr Thr Asn Leu Val Asp Leu Val Trp
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 Gly Ser Glu Arg Pro Pro Val Pro Asn Gln Pro Ile Tyr Ala Leu Gln
 195 200 205
 Glu Ala Phe Thr Gly Ser Thr Trp Gln Glu Lys Val Ser Gly Val Arg
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 Ser Gln Met Gln Lys His Gln Lys Val Pro Thr Ala Val Leu Leu Ser
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 Ala Leu Glu Glu Thr Ala Trp Leu Phe Asn Leu Arg Ala Ser Asp Ile
 245 250 255
 Pro Tyr Asn Pro Phe Phe Tyr Ser Tyr Thr Leu Leu Thr Asp Ser Ser
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 Ile Arg Leu Phe Ala Asn Lys Ser Arg Phe Ser Ser Glu Thr Leu Ser
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 Tyr Leu Asn Ser Ser Cys Thr Gly Pro Met Cys Val Gln Ile Glu Asp
 290 295 300
 Tyr Ser Gln Val Arg Asp Ser Ile Gln Ala Tyr Ser Leu Gly Asp Val
 305 310 315 320
 Arg Ile Trp Ile Gly Thr Ser Tyr Thr Met Tyr Gly Ile Tyr Glu Met
 325 330 335
 Ile Pro Arg Glu Lys Leu Val Thr Asp Thr Tyr Ser Pro Val Met Met
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 Thr Lys Ala Val Lys Asn Ser Lys Glu Gln Ala Leu Leu Lys Ala Ser
 355 360 365
 His Val Arg Asp Ala Val Ala Val Ile Arg Tyr Leu Val Trp Leu Glu
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 Lys Asn Val Pro Lys Gly Thr Val Asp Glu Phe Ser Gly Ala Glu Ile
 385 390 395 400
 Val Asp Lys Phe Arg Gly Glu Glu Gln Phe Ser Ser Gly Pro Ser Phe
 405 410 415

Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser
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 Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu
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 Asp Ala Gly Leu Asn Tyr Gly His Gly Thr Gly His Gly Ile Gly Asn
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 Ala Met Ala Lys Gly Met Phe Thr Ser Ile Glu Pro Gly Tyr Tyr Lys
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 Asp Gly Glu Phe Gly Ile Arg Leu Glu Asp Val Ala Leu Val Val Glu
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 Ala Lys Thr Lys Tyr Pro Gly Glu Leu Pro Asp Leu Val Val Ser Phe
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 Val Pro Tyr Asp Arg Asn Leu Ile Asp Val Ser Leu Leu Ser Pro Glu
 595 600 605
 His Leu Gln Tyr Leu Asn Arg Tyr Tyr Gln Thr Ile Arg Glu Lys Val
 610 615 620
 Gly Pro Glu Leu Gln Arg Arg Gln Leu Leu Glu Glu Phe Glu Trp Leu
 625 630 635 640
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Val

<210> 848
 <211> 1082
 <212> DNA
 <213> homo sapiens

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gctccagaag	cctgggacct	gctgcacaga
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ttcttcggcc	tcttagggaa	cctttttgtc
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240		
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300		
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ctctgccctg	tcatacaagg	ggtcatcaag
360		
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720		
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acagcgctga	tcctcacgct	cgtggttgcc
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tttgcttccc	tggaaattct	attccagggt
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1082		

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			20					25					30		
Trp	Asp	Leu	Leu	His	Arg	Val	Leu	Pro	Thr	Phe	Ile	Ile	Ser	Ile	Cys
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Phe	Phe	Gly	Leu	Leu	Gly	Asn	Leu	Phe	Val	Leu	Leu	Val	Phe	Leu	Leu

50

55

60

Pro Arg Arg Gln Leu Asn Val Ala Glu Ile Tyr Leu Ala Asn Leu Ala
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Ala Ser Asp Leu Val Phe Val Leu Gly Leu Pro Phe Trp Ala Glu Asn
85 90

Ile Trp Asn Gln Phe Asn Trp Pro Phe Gly Ala Leu Leu Cys Arg Val
100 105 110

Ile Asn Gly Val Ile Lys Ala Asn Leu Phe Ile Ser Ile Phe Leu Val
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Val Ala Ile Ser Gln Asp Arg Tyr Arg Val Leu Val His Pro Met Ala
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Ser Gly Arg Gln Gln Arg Arg Arg Gln Ala Arg Val Thr Cys Val Leu
145 150 155 160

Ile Trp Val Val Gly Gly Leu Leu Ser Ile Pro Thr Phe Leu Leu Arg
165 170 175

Ser Ile Gln Ala Val Pro Asp Leu Asn Ile Thr Ala Cys Ile Leu Leu
180 185 190

Leu Pro His Glu Ala Trp His Phe Ala Arg Ile Val Glu Leu Asn Ile
195 200 205

Leu Gly Phe Leu Leu Pro Leu Ala Ala Ile Val Phe Phe Asn Tyr His
210 215 220

Ile Leu Ala Ser Leu Arg Thr Arg Glu Glu Val Ser Arg Thr Arg Val
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Gln Gly Pro Lys Asp Ser Lys Thr Thr Ala Leu Ile Leu Thr Leu Val
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Val Ala Phe Leu Val Cys Trp Ala Pro Tyr His Phe Phe Ala Phe Leu
260 265 270

Glu Phe Leu Phe Gln Val Gln Ala Val Arg Gly Cys Phe Trp Glu Asp
275 280 285

Phe Ile Asp Leu Gly Leu Gln Leu Ala Asn Phe Phe Ala Phe Thr Asn
290 295 300

Ser Ser Leu Asn Pro Val Ile Tyr Val Phe Val Gly Arg Leu Phe Arg
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Thr Lys Val Trp Glu Leu Tyr Lys Gln Cys Thr Pro Lys Ser Leu Ala
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Pro Ile Ser Ser Ser His Arg Lys Glu Ile Phe Gln Leu Phe Trp Arg
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Asn

<210> 850
 <211> 3733
 <212> DNA
 <213> homo sapiens

<400> 850
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<400> 851

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 Gln Val Glu Trp Leu Gly Trp Leu Asn Thr Ile Gln Pro Pro Phe Leu
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 Trp Val Leu Phe Val Leu Ala Thr Leu Glu Asn Ile Phe Val Leu Ser
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 Val Phe Cys Leu His Lys Ser Ser Cys Thr Val Ala Glu Ile Tyr Leu
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 Gly Asn Leu Ala Ala Ala Asp Leu Ile Leu Ala Cys Gly Leu Pro Phe
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Lys Thr Met Ser Met Gly Arg Met Arg Gly Val Arg Trp Ala Lys Leu
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<210> 852

<211> 1284

<212> DNA

<213> homo sapiens

<400> 852

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ttgccctgct	cggtgctacg	gatggattac	aaaggagacg	caaccgtgtt	tttcattctc	840
cctaaccaag	gcaaaatgag	ggagattgaa	gaggttctga	ctccagagat	gctaattgag	900
tggaacaact	tgttgcggaa	gaggaatctt	tacaagaagc	tagagttgca	tcttcccaag	960
ttctccattt	ctggctccta	tgtattagat	cagattttgc	ccaggctggg	cttcacggat	1020
ctgttctcca	agtgggctga	cttatccggc	atcaccaaac	agcaaaaact	ggaggcatcc	1080
aaaagtcttc	acaagggcac	cttggacgtg	gatgaggctg	gcaccgaggc	tgacgcagcc	1140
acgacgttgc	cgatcaaatt	cttctctgcc	cagaccaatc	gccacatcct	gcgattcaac	1200
cggcccttcc	ttgtggtgat	cttttccacc	agcaccacga	gtgtcctctt	tctgggcaag	1260
gtcgtcgacc	ccacgaaacc	atag				1284

<210> 853
 <211> 427
 <212> PRT
 <213> homo sapiens

<400> 853

Met	His	Leu	Ile	Asp	Tyr	Leu	Leu	Leu	Leu	Val	Gly	Leu	Leu	Ala
1			5					10					15	
Leu	Ser	His	Gly	Gln	Leu	His	Val	Glu	His	Asp	Gly	Glu	Ser	Cys
			20					25					30	
Asn	Ser	Ser	His	Gln	Gln	Ile	Leu	Glu	Thr	Gly	Glu	Gly	Ser	Pro
			35				40				45			
Leu	Lys	Ile	Ala	Pro	Ala	Asn	Ala	Asp	Phe	Ala	Phe	Arg	Phe	Tyr

50	55	60
Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu		
65	70	75
Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His		
	85	90
Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu		
	100	105
Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu		
	115	120
Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe		
	130	135
Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met		
	145	150
Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val		
	165	170
Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly		
	180	185
Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val		
	195	200
Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile		
	210	215
Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr		
	225	230
Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu		
	245	250
His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly		
	260	265
Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu		
	275	280
Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu		
	290	295
Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys		
	305	310
Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu		
	325	330
Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr		
	340	345
Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu		

355

360

365

Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala
370 375 380

Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn
385 390 395 400

Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu
405 410 415

Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro
420 425

<210> 854

<211> 1284

<212> DNA

<213> homo sapiens

<400> 854

atgcatctta tcgactacct gctcctcctg ctgggtggag tactggccct ttctcatggc 60

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gagacagggt agggctcccc cagcctcaag atagcccctg ccaatgctga ctttgccttc 180

cgctcttact acctgatcgc ttccggagacc ccggggaaga acatcttttt ctccccgctg 240

agcatctcgg cggcctacgc catgctttcc ctgggggcct gctcacacag ccgcagccag 300

atccttgagg gcctgggctt caacctcacc gagctgtctg agtccgatgt ccataggggc 360

ttccagcacc tcttcgcacc tctcaacctc cccggccatg ggctggaaac atgcgtgggc 420

agtgtctctg tcttgagcca caacctgaag ttctctgcaa aattcctgaa tgacaccatg 480

gccgtctatg aggctaaact cttccacacc aactttctac aactgtggg cacaatccag 540

cttatcaacg accacgtcaa gaaggaaact cgagggaaga ttgtggattt ggtcagtgag 600

ctcaagaagg acgtcttgat ggtgctgggt aattacattt acttcaaagc cctgtgggag 660

aaaccattca tttcctcaag gaccactccc aaagactttt atgttgatga gaacacaaca 720

gtccgggtgc ccatgatgct gcaggaccag gaggatcact ggtatcttca tgacagatac 780

ttgcctgctc cggtgctacg gatggattac aaaggagacg caaccgtgtt ttctattctc 840

cctaaccaag gcaaaatgag ggagattgaa gaggttctga ctccagagat gctaattgag 900

tggaacaact tggtgcggaa gaggaatttt tacaagaagc tagagttgca tcttcccaag 960

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aaaagtttcc acaaggccac cttggacgtg gatgaggctg gcaccgaggc tgcagcagcc 1140

accacgttcc cgatcaaatt cttctctgcc cagaccaatc gccacatcct gogattcaac 1200
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 gtcgtcgacc ccacgaatac atag 1284

<210> 855
 <211> 427
 <212> PRT
 <213> homo sapiens

<400> 855

Met His Leu Ile Asp Tyr Leu Leu Leu Leu Val Gly Leu Leu Ala
 1 5 10 15
 Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser
 20 25 30
 Asn Ser Ser His Gln Gln Ile Leu Thr Gly Glu Gly Ser Pro Ser
 35 40 45
 Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr
 50 55 60
 Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu
 65 70 75 80
 Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His
 85 90 95
 Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu
 100 105 110
 Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu
 115 120 125
 Asn Leu Pro Gly His Gly Leu Glu Thr Cys Val Gly Ser Ala Leu Phe
 130 135 140
 Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met
 145 150 155 160
 Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val
 165 170 175
 Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly
 180 185 190
 Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val
 195 200 205
 Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile
 210 215 220

Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr
 225 230 235 240
 Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu
 245 250 255
 His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly
 260 265 270
 Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu
 275 280 285
 Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu
 290 295 300
 Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys
 305 310 315 320
 Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu
 325 330 335
 Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr
 340 345 350
 Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu
 355 360 365
 Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Thr Phe Ala
 370 375 380
 Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn
 385 390 395 400
 Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu
 405 410 415
 Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro
 420 425

<210> 856
 <211> 3428
 <212> DNA
 <213> homo sapiens

<220>
 <221> misc_feature
 <222> (711)..(711)
 <223> wherein N is either an "T" or a "C".

<220>
 <221> misc_feature
 <222> (2085)..(2085)
 <223> wherein N is either an "C" or a "G".

<400> 856

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tgccccacct	ggctcccaaa	accctccaaa	acaaaagacc	agaaaagcac	tctccaccca	120
gcagccaaac	gcctccttct	tgacgcgcagc	ccccaccctc	tgtctgctcg	agcccaggaa	180
aggcctgaag	gaacaggccg	gggaaggagc	cctccctctc	tccttctgct	ctccatccac	240
ccagcgcccg	catctggaga	ccctatggcc	cgggctcact	ggggctgctg	ccccggctg	300
gtctcctct	gtgcttgtgc	ctggggccac	acaaagccac	tggaccttgg	agggcaggat	360
gtgagaaatt	gttccaccaa	ccccctttac	cttccagtta	ctgtgggtcaa	taccacaatg	420
tcactcacag	ccctccgcca	gcagatgcag	accagaatc	tctcagccta	catcatccca	480
ggcacagatg	ctcacatgaa	gcagtacatc	ggccaacatg	acgagaggcg	tgcgtggatt	540
acaggcttta	cagggtctcg	aggaactgca	gtgggtgacta	tgaagaaagc	agctgtctgg	600
accgacagtc	gctactggac	tcaggctgag	cggcaaatgg	actgtaattg	ggagctccat	660
aaggaaattg	gcaccactcc	tattgtcacc	tggtcctcca	ccgagattcc	ngctggaggg	720
cgtgtgggtt	ttgaccttct	cctcttctgc	attgacacct	gggagagtta	tgtatctggc	780
ctccaaggct	ctaacagaca	gctgggtgtc	atcacaacca	atcttctgga	cctgggatgg	840
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gtcccgaact	ccgtccttct	gtcggcgctt	gaggagacgg	cctggctctt	caacctctga	1020
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gatgctggtc	tcaattatgg	tcatgggaca	ggccacggca	ttggcaactt	cctgtgtgtg	1860
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cagggtctct	tggccccaga	tggcacctcc	ctgcaccccg	gggtgtgata	ccacaccttg	2520
ggcccccaat	cccaggcccc	gaaataggaa	agccagctag	tctcttctct	tctgtgatct	2580
cagtaggcct	aacctataac	ctaacacaga	ctgctacagc	tgctccccct	ccgccaaaca	2640
aagccccaa	aaaacaatgc	cctaccacc	caaggtgtcc	atggtcccg	gaaaaccaca	2700
cctgtcacgc	cggtttgggc	gtaaccagaa	ctgttcccc	ccaccagggc	ttaaaaatcg	2760
ccccacttt	ttaaccatcg	tccattaacc	acctggtggg	catagccaga	gctgttcgaa	2820
cccagccagg	gatgaaaaat	caacccccga	catggaacct	atgattccta	aacccggggt	2880
aggttccatg	ccaagtaaca	gcagaggggg	ttaagccata	ggaatttggc	tgtggagtaa	2940
gagggaatgc	ggtgaggcag	tgtggaatat	gacctaccac	gagggtggag	aacaaacttg	3000
ggcagccgga	accgctcaat	attttagatt	cctggcattc	gaggagccct	ttgaactttc	3060
caaagtgcag	ccacagctac	aatgctgtta	aatcctccca	cattttcttg	atgcccttcc	3120
acctgtgtgt	gacagtgtct	ggtttcccca	ttttacagac	aggaaaaactg	agcttcagac	3180
aggggggtgg	ctttgcttaa	ggacacacaa	atttggttgg	gagttgatgg	ggccagatga	3240
gccagcattc	cagctgtttc	acccttcagc	aacatgcaga	gtccctgagc	ccacctccca	3300
gccctctcct	cattctctga	accactgtgt	gtgagaagaa	tttgcctccg	ccaaattggc	3360
cgttagccac	ctgggtccac	atcctgctaa	gacgttttaa	acagcctaac	aaagacactt	3420

<210> 857
 <211> 673
 <212> PRT
 <213> homo sapiens

<400> 857

Met Ala Arg Ala His Trp Gly Cys Cys Pro Trp Leu Val Leu Leu Cys
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Ala Cys Ala Trp Gly His Thr Lys Pro Leu Asp Leu Gly Gly Gln Asp
 20 25 30

Val Arg Asn Cys Ser Thr Asn Pro Pro Tyr Leu Pro Val Thr Val Val
 35 40 45

Asn Thr Thr Met Ser Leu Thr Ala Leu Arg Gln Gln Met Gln Thr Gln
 50 55 60

Asn Leu Ser Ala Tyr Ile Ile Pro Gly Thr Asp Ala His Met Asn Glu
 65 70 75 80

Tyr Ile Gly Gln His Asp Glu Arg Arg Ala Trp Ile Thr Gly Phe Thr
 85 90 95

Gly Ser Ala Gly Thr Ala Val Val Thr Met Lys Lys Ala Ala Val Trp
 100 105 110

Thr Asp Ser Arg Tyr Trp Thr Gln Ala Glu Arg Gln Met Asp Cys Asn
 115 120 125

Trp Glu Leu His Lys Glu Val Gly Thr Thr Pro Ile Val Thr Trp Leu
 130 135 140

Leu Thr Glu Ile Pro Ala Gly Gly Arg Val Gly Phe Asp Pro Phe Leu
 145 150 155 160

Leu Ser Ile Asp Thr Trp Glu Ser Tyr Asp Leu Ala Leu Gln Gly Ser
 165 170 175

Asn Arg Gln Leu Val Ser Ile Thr Thr Asn Leu Val Asp Leu Val Trp
 180 185 190

Gly Ser Glu Arg Pro Pro Val Pro Asn Gln Pro Ile Tyr Ala Leu Gln
 195 200 205

Glu Ala Phe Thr Gly Ser Thr Trp Gln Glu Lys Val Ser Gly Val Arg
 210 215 220

Ser Gln Met Gln Lys His Gln Lys Val Pro Thr Ala Val Leu Leu Ser
 225 230 235 240

Ala Leu Glu Glu Thr Ala Trp Leu Phe Asn Leu Arg Ala Ser Asp Ile
 245 250 255

Pro Tyr Asn Pro Phe Phe Tyr Ser Tyr Thr Leu Leu Thr Asp Ser Ser
 260 265 270
 Ile Arg Leu Phe Ala Asn Lys Ser Arg Phe Ser Ser Glu Thr Leu Ser
 275 280 285
 Tyr Leu Asn Ser Ser Cys Thr Gly Pro Met Cys Val Gln Ile Glu Asp
 290 295 300
 Tyr Ser Gln Val Arg Asp Ser Ile Gln Ala Tyr Ser Leu Gly Asp Val
 305 310 315 320
 Arg Ile Trp Ile Gly Thr Ser Tyr Thr Met Tyr Gly Ile Tyr Glu Met
 325 330 335
 Ile Pro Arg Glu Lys Leu Val Thr Asp Thr Tyr Ser Pro Val Met Met
 340 345 350
 Thr Lys Ala Val Lys Asn Ser Lys Glu Gln Ala Leu Leu Lys Ala Ser
 355 360 365
 His Val Arg Asp Ala Val Ala Val Ile Arg Tyr Leu Val Trp Leu Glu
 370 375 380
 Lys Asn Val Pro Lys Gly Thr Val Asp Glu Phe Ser Gly Ala Glu Ile
 385 390 395 400
 Val Asp Lys Phe Arg Gly Glu Glu Gln Phe Ser Ser Gly Pro Ser Phe
 405 410 415
 Glu Thr Ile Ser Ala Ser Gly Leu Asn Ala Ala Leu Ala His Tyr Ser
 420 425 430
 Pro Thr Lys Glu Leu Asn Arg Lys Leu Ser Ser Asp Glu Met Tyr Leu
 435 440 445
 Leu Asp Ser Gly Gly Gln Tyr Trp Asp Gly Thr Thr Asp Ile Thr Arg
 450 455 460
 Thr Val His Trp Gly Thr Pro Ser Ala Phe Gln Lys Glu Ala Tyr Thr
 465 470 475 480
 Arg Val Leu Ile Gly Asn Ile Asp Leu Ser Arg Leu Ile Phe Pro Ala
 485 490 495
 Ala Thr Ser Gly Arg Met Val Glu Ala Phe Ala Arg Arg Ala Leu Trp
 500 505 510
 Asp Ala Gly Leu Asn Tyr Gly His Gly Thr Gly His Gly Ile Gly Asn
 515 520 525
 Phe Leu Cys Val His Glu Trp Pro Val Gly Phe Gln Ser Asn Asn Ile
 530 535 540
 Ala Met Ala Lys Gly Met Phe Thr Ser Ile Glu Pro Gly Tyr Tyr Lys
 545 550 555 560

Asp Gly Glu Phe Gly Ile Arg Leu Glu Asp Val Ala Leu Val Val Glu
565 570 575

Ala Lys Thr Lys Tyr Pro Gly Glu Leu Pro Asp Leu Val Val Ser Phe
580 585 590

Val Pro Tyr Asp Arg Asn Leu Ile Asp Val Ser Leu Leu Ser Pro Glu
595 600 605

His Leu Gln Tyr Leu Asn Arg Tyr Tyr Gln Thr Ile Arg Glu Lys Val
610 615 620

Gly Pro Glu Leu Gln Arg Arg Gln Leu Leu Glu Glu Phe Glu Trp Leu
625 630 635 640

Gln Gln His Thr Glu Pro Leu Ala Ala Arg Ala Pro Asp Thr Ala Ser
645 650 655

Trp Ala Ser Val Leu Val Val Ser Thr Leu Ala Ile Leu Gly Trp Ser
660 665 670

Val

<210> 858
<211> 19
<212> DNA
<213> homo sapiens

<400> 858
gagccgggta aggtctggt

19

<210> 859
<211> 19
<212> DNA
<213> homo sapiens

<400> 859
gctaggggct tcggacctt

19

<210> 860
<211> 19
<212> DNA
<213> homo sapiens

<400> 860
aacaggatgt cccaacagg

19

<210> 861
<211> 19
<212> DNA
<213> homo sapiens

<400> 861
tccaggaact gagtgccaa 19

<210> 862
<211> 19
<212> DNA
<213> homo sapiens

<400> 862
catggtccca ggagagccc 19

<210> 863
<211> 17
<212> DNA
<213> homo sapiens

<400> 863
cctgttgggc atagcca 17

<210> 864
<211> 19
<212> DNA
<213> homo sapiens

<400> 864
ccctccagca ggaatctcg 19

<210> 865
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<213> homo sapiens

<400> 865
acaaggtgca ggggccgca 19

<210> 866
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<212> DNA
<213> homo sapiens

<400> 866
gtgggccctg tataatcac 19

<210> 867
<211> 19
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<213> homo sapiens

<400> 867
ctcaagggtc caagtgtac 19

<210> 868
 <211> 19
 <212> DNA
 <213> homo sapiens

<400> 868
 acaagtatca ggtaatggc

19

<210> 869
 <211> 19
 <212> DNA
 <213> homo sapiens

<400> 869
 cctctcttat tacacttcc

19

<210> 870
 <211> 19
 <212> DNA
 <213> homo sapiens

<400> 870
 gttgtgaggg ttaaaggca

19

<210> 871
 <211> 19
 <212> DNA
 <213> homo sapiens

<400> 871
 ggcacggagt cctcacgaa

19

<210> 872
 <211> 19
 <212> DNA
 <213> homo sapiens

<400> 872
 aactgacctg agtacagtg

19

<210> 873
 <211> 19
 <212> DNA
 <213> homo sapiens

<400> 873
 ctgacctgag tacagtga

19

<210> 874
 <211> 19

<212> DNA
 <213> homo sapiens
 <400> 874
 tctgctccat ggagctatt 19

<210> 875
 <211> 19
 <212> DNA
 <213> homo sapiens
 <400> 875
 atttctagac ctcagtgtc 19

<210> 876
 <211> 19
 <212> DNA
 <213> homo sapiens
 <400> 876
 gaccgtctcg tcgaacagc 19

<210> 877
 <211> 13
 <212> DNA
 <213> homo sapiens
 <400> 877
 gaagctgggtg gct 13

<210> 878
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<210> 879
 <211> 16
 <212> DNA
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 <400> 879
 ggtaccggtt tcataa 16

<210> 880
 <211> 18
 <212> DNA
 <213> homo sapiens

<400> 880
atgtagatag tcttctgg 18

<210> 881
<211> 14
<212> DNA
<213> homo sapiens

<400> 881
ccagatgcag ctag 14

<210> 882
<211> 14
<212> DNA
<213> homo sapiens

<400> 882
cttctgacac agct 14

<210> 883
<211> 16
<212> DNA
<213> homo sapiens

<400> 883
aagtacatga agaatt 16

<210> 884
<211> 19
<212> DNA
<213> homo sapiens

<400> 884
gagccgggtg aggtctggt 19

<210> 885
<211> 19
<212> DNA
<213> homo sapiens

<400> 885
gctaggggcc tcggacctt 19

<210> 886
<211> 19
<212> DNA
<213> homo sapiens

<400> 886
aacaggatgc cccaacagg 19

<210> 887
 <211> 19
 <212> DNA
 <213> homo sapiens

<400> 887
 tccaggaacc gagtgcctaa 19

<210> 888
 <211> 19
 <212> DNA
 <213> homo sapiens

<400> 888
 catggtcccc ggagagccc 19

<210> 889
 <211> 17
 <212> DNA
 <213> homo sapiens

<400> 889
 cctgttgggt atagcca 17

<210> 890
 <211> 19
 <212> DNA
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ggagaccaag gttccagctc 20

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gctgaaagac cagaacaaga attc 24

<210> 1228
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<400> 1228
tggaagagtt tgtaaccag ataatac 26

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	<400> 1241	
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	<223> wherein "n" equals a C3 phosphoramidite linker.	
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	<210> 1243	
	<211> 25	
	<212> DNA	
	<213> Homo sapiens	
	<400> 1243	
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	<210> 1244	
	<211> 22	
	<212> DNA	
	<213> Homo sapiens	
	<220>	
	<221> misc_feature	
	<222> (12)..(12)	
	<223> wherein "n" equals a C3 phosphoramidite linker.	
	<400> 1244	
	tggaagccca gnccccagag gt	22
	<210> 1245	
	<211> 25	
	<212> DNA	
	<213> Homo sapiens	
	<400> 1245	
	agcccaggcc ccagaggtyc tccca	25
	<210> 1246	
	<211> 27	
	<212> DNA	
	<213> Homo sapiens	

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<222> (12)..(12)
<223> wherein "n" equals a C3 phosphoramidite linker.

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<220>
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<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

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<400> 1246
aatgttgaga angncagcct aaccctg

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27

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<210> 1247
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<223> wherein "n" equals a C3 phosphoramidite linker.

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<220>
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<222> (21)..(21)
<223> wherein "n" equals a C3 phosphoramidite linker.

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<400> 1247
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27

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<210> 1248
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<220>
<221> misc_feature
<222> (12)..(12)
<223> wherein "n" equals a C3 phosphoramidite linker.

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<400> 1248
agaaaagctt gntcaggca gatcagc

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27

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<210> 1249
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<400> 1249
tacctaaata aataataaaa gccag 25

<210> 1250
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<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

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<210> 1251
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<223> wherein "n" equals a C3 phosphoramidite linker.

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agacttcacc tcttggcanc ttggctt 27

<210> 1252
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<212> DNA
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<400> 1252
ctgcatgttg ctgaaggggtg aaaga 25

<210> 1253
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<212> DNA
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<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (16)..(16)

<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1253
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27

<210> 1254
<211> 27
<212> DNA
<213> Homo sapiens

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<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

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ttaccctang gctgacctnc caggaac

27

<210> 1255
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1255
tcacctggct cctcaccgag attcc

25

<210> 1256
<211> 27
<212> DNA
<213> Homo sapiens

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<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
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<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1256
tatttcagnc cactgacang gcctcag

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<210> 1257
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 <212> DNA
 <213> Homo sapiens

 <400> 1257
 accttcataag aggggtataat aaaag 25

<210> 1258
 <211> 25
 <212> DNA
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 <400> 1258
 aagagtttgt ttgaggaaag ggttt 25

<210> 1259
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 <212> DNA
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 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> wherein "n" equals a C3 phosphoramidite linker.

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<210> 1260
 <211> 27
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> (15)..(15)
 <223> wherein "n" equals a C3 phosphoramidite linker.

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<210> 1261
 <211> 25

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<212> DNA
<213> Homo sapiens

<400> 1261
ccagtaattt atgtctttgt gggcc
25

<210> 1262
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1262
atcctgaatt atccaagtgg gccct
25

<210> 1263
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1263
cagcaggaaa caaataacaa gtatc
25

<210> 1264
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (18)..(18)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1264
acaagtatcr ggtaatgncc tctctta
27

<210> 1265
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1265
ctgggacctg ctgnacagag tgctgcc
27

<210> 1266
<211> 27

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<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (9)..(9)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
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<222> (11)..(11)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1266
tgaaccaana ngcttggtt tcttatac 27

<210> 1267
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1267
gagccctcct ctgccgtgtc atcaa 25

<210> 1268
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1268
agatctgaac atcaccgcct gcac 25

<210> 1269
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1269
cactgggcaa atcngcnggg ctcccc 27

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<210> 1270
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (3)..(3)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (16)..(16)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1270
 gtnggaatga caggtngaag ggagcca

27

<210> 1271
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (16)..(16)
 <223> wherein "n" equals a C3 phosphoramidite linker.

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27

<210> 1272
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 <212> DNA
 <213> Homo sapiens

<400> 1272
 taacagctca ttgagtcttk cacag

25

<210> 1273
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 <212> DNA
 <213> Homo sapiens

<400> 1273
 gggcagtcac tcagcaccag agcac

25

<210> 1274
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<212> DNA
<213> Homo sapiens

<400> 1274
ccctagaaga gtgtgaaaag gaatg
25

<210> 1275
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (15)..(15)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1275
attccttcac tcatntatna aacaaaa
27

<210> 1276
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1276
tacgttgagc gatgagcccc aggtt
25

<210> 1277
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (16)..(16)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1277
acaggggctg gggatngcna aatacac
27

<210> 1278
<211> 22
<212> DNA
<213> Homo sapiens

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<210> 1283
 <211> 22
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (13)..(13)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1283
 cattgcacca aacctggatg gc

22

<210> 1284
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (7)..(7)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1284
 gctttcnggt ggtgncagtg ccagtc

27

<210> 1285
 <211> 25
 <212> DNA
 <213> Homo sapiens

<400> 1285
 gagcgaaggg ctggctgagg tcatg

25

<210> 1286
 <211> 25
 <212> DNA
 <213> Homo sapiens

<400> 1286
 accttttgct tgatttttca ctgta

25

<210> 1287
 <211> 25

<212> DNA
<213> Homo sapiens

<400> 1287
ggctcccaat actgattctg ctcca

25

<210> 1288
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (18)..(18)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1288
acccacagca ccctgctnga ccgtctc

27

<210> 1289
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (16)..(16)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1289
agggttgcag ggaganctgg gatgagg

27

<210> 1290
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (11)..(11)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1290
gctgggatga ngyctggggt gctgcct

27

<210> 1291
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1291
gttctctgga gaaaaaactg tgctg 25

<210> 1292
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1292
ccccctctcc aagtctntgt ccacaa 27

<210> 1293
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1293
gaagaggga ctgaggcagg gacag 25

<210> 1294
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (15)..(15)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (18)..(18)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1294
aagggtgcta cgtanatntg aggcac 27

<210> 1295
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1295
cccagcgctg gggaaagaaa ggaca 25

<210> 1296
 <211> 25
 <212> DNA
 <213> Homo sapiens

<400> 1296
 gagatgcggt aggaagactg ttaag

25

<210> 1297
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (15)..(15)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1297
 aagcttgaan cctcnaggat gggttca

27

<210> 1298
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 1298
 aagctctacc acgccttctc ag

22

<210> 1299
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (13)..(13)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1299
 ggaacttgtn ctctgggtcc cagagca 27

<210> 1300
 <211> 25
 <212> DNA
 <213> Homo sapiens

<400> 1300
 tactggcgaa gacagcgcg atggg 25

<210> 1301
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 1301
 ccagcaggag agccaggacc ca 22

<210> 1302
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 1302
 ccaagcgcaa ggtgagcagg gg 22

<210> 1303
 <211> 22
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1303
 aggtcggacc ancttttccc aa 22

<210> 1304
 <211> 27
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (14)..(14)
 <223> wherein "n" equals a C3 phosphoramidite linker.

```

<220>
<221> misc_feature
<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

```

```

<220>
<221> misc_feature
<222> (20)..(20)
<223> wherein "n" equals a C3 phosphoramidite linker.

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<400> 1304
tccctatctt tgcnacnctn atgctgt

```

27

```

<210> 1305
<211> 27
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

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```

<400> 1305
accatactg acccttttng caagtcc

```

27

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<210> 1306
<211> 27
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (10)..(10)
<223> wherein "n" equals a C3 phosphoramidite linker.

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<220>
<221> misc_feature
<222> (21)..(21)
<223> wherein "n" equals a C3 phosphoramidite linker.

```

```

<400> 1306
agagcagttg gaggtcaggt ncaggga

```

27

```

<210> 1307
<211> 25
<212> DNA
<213> Homo sapiens

```

<400> 1307
caaaatcctg cctaatagtg agtgc

25

<210> 1308
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (8)..(8)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1308
tccttgtnac rcaggagtcc ccatccc

27

<210> 1309
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (10)..(10)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1309
gctgtgaagn tcgnggagtt gcccacc

27

<210> 1310
<211> 22
<212> DNA
<213> Homo sapiens

<400> 1310
aaggcrggga tggggactcc tg

22

<210> 1311
<211> 22
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (3)..(3)

<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1311
tgnggccacc ccagctgtgt ca

22

<210> 1312
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1312
atgtgtgtca cgttctgccca tcacc

25

<210> 1313
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1313
atctggaact tatagtnttg aaaagaa

27

<210> 1314
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (14)..(14)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1314
gaggggttcc agangtacnt atattta

27

<210> 1315
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1315
aagtagacaa ggaatgggtg tgaaa

25

<210> 1316
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (11)..(11)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (13)..(13)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (15)..(15)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1316
tcataatcac nantnaaant tagtagc

27

<210> 1317
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1317
gaaattttgc tgaagagaat gctaa

25

<210> 1318
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1318
cacatgtaaa tgactcagaa taatg

25

<210> 1319
<211> 27

```

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (16)..(16)
<223> wherein "n" equals a C3 phosphoramidite linker.

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27

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<400> 1319
ttcagttcta ggaatnatat cagacac

```

```

<210> 1320
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (9)..(9)
<223> wherein "n" equals a C3 phosphoramidite linker.

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<220>
<221> misc_feature
<222> (19)..(19)
<223> wherein "n" equals a C3 phosphoramidite linker.

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27

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<400> 1320
cttggtaana agcccatna attcttc

```

```

<210> 1321
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (3)..(3)
<223> wherein "n" equals a C3 phosphoramidite linker.

```

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<220>
<221> misc_feature
<222> (15)..(15)
<223> wherein "n" equals a C3 phosphoramidite linker.

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27

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<400> 1321
ggntggcacc gagngtcag cagccac

```

```

<210> 1322
<211> 27

```


<212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (7)..(7)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (12)..(12)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1322
 aacctcncg gncatgggct ggaaaca

27

<210> 1323
 <211> 27
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (2)..(2)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<220>
 <221> misc_feature
 <222> (18)..(18)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1323
 tntcttgac agatgttnat tatgaaa

27

<210> 1324
 <211> 27
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (9)..(9)
 <223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1324
 ccggactgnt gtgttctcat caacata

27

<210> 1325
 <211> 27

```

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

<220>
<221> misc_feature
<222> (20)..(20)
<223> wherein "n" equals a C3 phosphoramidite linker.

<400> 1325
gatcctggct tgttcantan tctaattg
27

<210> 1326
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1326
gaggggaagat tgtggatttg gtcag
25

<210> 1327
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1327
agaccctaaa ataaactctg aggat
25

<210> 1328
<211> 25
<212> DNA
<213> Homo sapiens

<400> 1328
taaaccatat aaagcactcc acaga
25

<210> 1329
<211> 27
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (10)..(10)
<223> wherein "n" equals a C3 phosphoramidite linker.

```

```

<220>
<221> misc_feature
<222> (17)..(17)
<223> wherein "n" equals a C3 phosphoramidite linker.

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<400> 1329
tatgaaacgn gtaccanttc tatcccc 27

```

```

<210> 1330
<211> 39
<212> DNA
<213> Homo sapiens

```

```

<400> 1330
tgtaaaacga cgGCCagtag ttctctctcc tccctcact 39

```

```

<210> 1331
<211> 39
<212> DNA
<213> Homo sapiens

```

```

<400> 1331
tgtaaaacga cgGCCagtgG cattcacagG tgatttcagt 39

```

```

<210> 1332
<211> 39
<212> DNA
<213> Homo sapiens

```

```

<400> 1332
tgtaaaacga cgGCCagttt ctgggcttta cctctctc 39

```

```

<210> 1333
<211> 39
<212> DNA
<213> Homo sapiens

```

```

<400> 1333
tgtaaaacga cgGCCagttt ctgggcttta cctctctc 39

```

```

<210> 1334
<211> 39
<212> DNA
<213> Homo sapiens

```

```

<400> 1334
tgtaaaacga cgGCCagtcC aggtgcagga ttaacagac 39

```

```

<210> 1335
<211> 39

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<212> DNA
 <213> Homo sapiens

 <400> 1335
 tgtaaaacga cggccagtag taggaacttg cacagtccg 39

 <210> 1336
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1336
 tgtaaaacga cggccagtag ccacaccta tctacacg 39

 <210> 1337
 <211> 38
 <212> DNA
 <213> Homo sapiens

 <400> 1337
 tgtaaaacga cggccagtag gtgagatctt gccactgc 38

 <210> 1338
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1338
 tgtaaaacga cggccagtag gccagacaat gatgtgatg 39

 <210> 1339
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1339
 tgtaaaacga cggccagtag tccaggtatg gtggcatgt 39

 <210> 1340
 <211> 37
 <212> DNA
 <213> Homo sapiens

 <400> 1340
 tgtaaaacga cggccagtag gaggaagca cgtgatg 37

 <210> 1341
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1341
tgtaaaacga cggccagttg taaagccctt tgcagaagt 39

<210> 1342
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1342
tgtaaaacga cggccagtct ctgaaaagcc ccagagaat 39

<210> 1343
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1343
tgtaaaacga cggccagtga ggctccagac tctcctggt 39

<210> 1344
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1344
tgtaaaacga cggccagtca ttgcctagaa acctttgca 39

<210> 1345
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1345
tgtaaaacga cggccagtag ccacagctac aatgctggt 39

<210> 1346
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1346
tgtaaaacga cggccagtct gccgtcaaca cagaactct 39

<210> 1347
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1347
tgtaaaacga cggccagtag aagaacagtt ctcctccgg 39

<210> 1348
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1348
 tgtaaaacga cggccagtcga tgccttgccct tgtactttc 39

<210> 1349
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1349
 tgtaaaacga cggccagtat ggaacacaga ggggttagg 39

<210> 1350
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1350
 tgtaaaacga cggccagtgg gttgtatacc acaccctgg 39

<210> 1351
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1351
 tgtaaaacga cggccagtgc agataggaaa gccagctag 39

<210> 1352
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1352
 tgtaaaacga cggccagtcga cttgtggaaa gcacacaga 39

<210> 1353
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1353
 tgtaaaacga cggccagtag gaaatttgag gccatcact 39

<210> 1354
 <211> 39

<212> DNA
 <213> Homo sapiens

 <400> 1354
 tgtaaaacga cggccagtag cagtcaagat cccttccat 39

 <210> 1355
 <211> 38
 <212> DNA
 <213> Homo sapiens

 <400> 1355
 tgtaaaacga cggccagtga aagagccctc cctctctc 38

 <210> 1356
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1356
 tgtaaaacga cggccagtca aggtggacag tcttcggta 39

 <210> 1357
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1357
 tgtaaaacga cggccagttc ctcatagcag ccctattga 39

 <210> 1358
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1358
 tgtaaaacga cggccagtat ccgaagacag ggagttcat 39

 <210> 1359
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1359
 tgtaaaacga cggccagtat ccgaagacag ggagttcat 39

 <210> 1360
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1360
tgtaaaacga cggccagttc ttgccttcc tggaattct 39

<210> 1361
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1361
tgtaaaacga cggccagtcg tcccagatct gaacatcac 39

<210> 1362
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1362
tgtaaaacga cggccagtga accaagaagc ttggctttc 39

<210> 1363
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1363
tgtaaaacga cggccagtaa cttcccagac toaagggat 39

<210> 1364
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1364
tgtaaaacga cggccagtca agtgatcctc cactttggt 39

<210> 1365
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1365
tgtaaaacga cggccagtcc tccactttgg tctcccata 39

<210> 1366
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1366
tgtaaaacga cggccagtgc tgtagtctgc cacttcctg 39

<210> 1367
<211> 38
<212> DNA
<213> Homo sapiens

<400> 1367
tgtaaaacga cggccagtag gaccaaggtc tggaact 38

<210> 1368
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1368
tgtaaaacga cggccagtc ctggaacaca gaccattaa 39

<210> 1369
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1369
tgtaaaacga cggccagtaa ctcccagac tcaagggat 39

<210> 1370
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1370
tgtaaaacga cggccagtcc ctctgggca gagaatata 39

<210> 1371
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1371
tgtaaaacga cggccagtcc ctctgggca gagaatata 39

<210> 1372
<211> 36
<212> DNA
<213> Homo sapiens

<400> 1372
tgtaaaacga cggccagtc atcttctctgg tggtgg 36

<210> 1373
<211> 39

<212> DNA
 <213> Homo sapiens

 <400> 1373
 tgtaaaacga cggccagtcg tcccagatct gaacatcac 39

 <210> 1374
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1374
 tgtaaaacga cggccagtggt ggtctttaa ggaggcctg 39

 <210> 1375
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1375
 tgtaaaacga cggccagtggt tctcagcact gtgatcctc 39

 <210> 1376
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1376
 tgtaaaacga cggccagtgc gggagttgta acaaatgct 39

 <210> 1377
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1377
 tgtaaaacga cggccagtgc tatgcaaaaa cctcatcca 39

 <210> 1378
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1378
 tgtaaaacga cggccagtca tctacacat gcatagggc 39

 <210> 1379
 <211> 39
 <212> DNA
 <213> Homo sapiens

<400> 1379
tgtaaaacga cggccagtta gcctctccag ttctagccc 39

<210> 1380
<211> 40
<212> DNA
<213> Homo sapiens

<400> 1380
tgtaaaacga cggccagtaa taaaagaggt gctgaccac 40

<210> 1381
<211> 38
<212> DNA
<213> Homo sapiens

<400> 1381
tgtaaaacga cggccagtcc accatgaccc aagtttat 38

<210> 1382
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1382
tgtaaaacga cggccagtga ggaatccctt tgactcac 39

<210> 1383
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1383
tgtaaaacga cggccagtgt gttccttcaa ctgttgtcc 39

<210> 1384
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1384
tgtaaaacga cggccagtgt ggtctttaa ggaggcctg 39

<210> 1385
<211> 39
<212> DNA
<213> Homo sapiens

<400> 1385
tgtaaaacga cggccagtag atgtatggcg gaggtttct 39

<210> 1386
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1386
 tgtaaaacga cggccagttt ttggatgtaa acagtgggc 39

<210> 1387
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1387
 tgtaaaacga cggccagtgg aagcccatg tgaataaat 39

<210> 1388
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1388
 tgtaaaacga cggccagtac ttcagtcgct ccttggtac 39

<210> 1389
 <211> 39
 <212> DNA
 <213> Homo sapiens

 <400> 1389
 tgtaaaacga cggccagtgc tccatctgaa tgggttctg 39

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